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Minimum
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                                                                                                                                                                                                                                                                                                                                                                                                                  Title:
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2668
1 MNRGVPFRHLLLVL
   8 7 6 5 4
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1: geneseqp1980s:*
2: geneseqp1990s:*
3: geneseqp2000s:*
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                                                                                                                                                             summaries
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1693.744 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	œ	7	o,	s	4	ω	N	_	Result No.
1064	1064	1064	1064	1064	1064	1064	1064	1064	1064	1064	1064	1064	1064	1064	1064	1064	1064	1064	1064	1064	1064	1064	1064	2651.5	Score
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AAY59169	AAY51079	AAB19508	AAP93009	AAY59172	AAY51082	AAR20152	AAY59171	AAY51081	AAB19510	AAY59170	ADA44807	ADP12495	ADE57489	ADD25609	AAG79087	AAB81502	AAY88329	AAY51080	AAB19509	AAY88328	AAY39825	AAR07606	AAR07605	AAB00158	ID
Aay59169 CD4-Ig fu	Aay51079 Human fus	Aab19508 CD4-IgG1		Aay59172 CD4-Ig fu	Aay51082 Human fus	Human	Aay59171 CD4-Ig fu	Aay51081 Human fus		Aay59170 CD4-Ig fu		Adp12495 Protein e		Add25609 Binding d		Aab81502 Human CD4	Aay88329 T4 glycop	Aay51080 Human fus	Aab19509 CD4-IgM f	Aay88328 T4 glycop	Aay39825 Soluble h	Aar07606 Plasmid T	Aar07605 Plasmid T	58 sC	Description

45	44	43	42	41	40	39	38	37	36	ა 5	υ 4	ω u	32	4	30	29	28	27	4
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39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.7	39.8	39.9	39.9	39.9	39.9
462	462	462	462	462	458	458	458	458	458	402	402	400	398	398	458	729	729	729	123
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AAW83142	AAW02214	AAR89457	AAR78677	AAR27277	AAB07769	AAY39826	AAR13491	AAP91369	AAP81990	AAP94757	AAP91922	AAR06374	AAR89450	AAR78673	ADE65841	AAY59168	AAY51078	AAB19507	MARSSOUG
Aaw83142	Aaw02214	Aar89457	Aar78677	Aar27277	Aab07769	Aay39826	Aar13491	Aap91369	Aap81990	Aap94757	Aap91922	Aar06374	Aar89450	Aar78673	Ade65841	Aay59168	Aay51078	Aab19507	hapsood
Chimeric	CD4:Fc re	CD4:gamma	T-cell re	CD4:eta p	DNA encod	Soluble h	Human CD4	T4 protei	Clone pT4	Sequence	Sequence	Truncated	CD4 D1-D4	CD4 domai	Human CD4	CD4-Ig fu	Human fus	CD4-IgG1	Gerrent C

ALIGNMENTS

AAB00158; AAB00158 standard; protein; 507 \$

sCD4-SCFv(17b) HIV single chain antibody fusion protein. 08-FEB-2001 (first entry)

Fusion protein; HIV; human immunodeficiency virus; antibody; Fv; AIDS; acquired immune deficiency syndrome; neutralisation; infection; gene therapy; CD4; gp120; glycoprotein; resistance; vaccination; binding domain; single chain antibody; chimera; chimeric protein.

Synthetic. Human immunodeficiency virus.

WO200055207-A1.

21-SEP-2000

16-MAR-2000; 2000WO-US006946.

16-MAR-1999; 99US-0124681P

(USSH) US NAT INST OF HEALTH

EA,

Del Castillo

Ω .

WPI; 2000-638183/61. N-PSDB; AAA54045.

Novel neutralizing bispecific fusion proteins effective in viral such as HIV neutralization, comprises two different binding domains, inducing-binding domain and induced-binding domain functionally linked by linker.

Claim 39; Page 46-47; 55pp; English.

RESULT 1
AABOOLS8
ID AABO
XX AABO
XX AABO
XX AABO
XX Pusi
IKW Pusi
KW Sene
KW sCD4-SCFv(17b) is a neutralising bispecific fusion protein capable of binding to two sites of its target protein. The protein comprises a first binding domain capable of binding to an inducing site on the target protein, a second binding domain capable of forming neutralising complex with an induced epitope of the target protein and a linker connecting the binding domains. sCD4-SCFv(17b) comprises a soluble CD4 fragment (containing domains D1 and D2) fused to a single chain Fv portion of antibody 17b via a linker. sCD4-SCFv(17b), its variant, analogue or mimetic is used for inactivating gp120 protein of HIV, and for

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           neutralising HIV. It is also used for blocking and preventing the binding of the viral or recombinant gp120 protein to soluble CD4 or lymphocyte CD4 and for inhibiting HIV replication. The chimeric proteins is therefore useful for treating HIV infection and also AIDS. It is are particularly useful in the prevention of infection during or immediately after HIV exposure (e.g., mother/infant transmission, post-exposure prophylaxis, and as a topical inhibitor) and for providing long term resistance to HIV infections and AIDS. Gene therapy is used to secrete the bispecific protein at mucosal surfaces, such as the vaginal, rectal or oral mucosa. The fusion proteins is highly potent, broadly cross-creactive with neutralising antibody with high in vivo activity and no Fc mediated undesirable targetting properties. When the fusion protein is substantially derived from human proteins, it has minimal immunogenicity and toxicity in humans which is of great value in prevention of infection of during or immediately after HIV exposure
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Best Local S
Matches 507
                                                               25-MAR-2003
09-JAN-2003
06-FEB-1991
Plasma
                        Plasmid T4/LFA-3/AD gene product with C-terminal encoding phosphatidylinositol (PI) linkage signaling sequence.
                                                                                                                   AAR07605;
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  affinity; micelle
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Pred. No. 9.4e-128;
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RESULT 3
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Best Local
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                 25-MAR-2003
09-JAN-2003
06-FEB-1991
                                                                                          AAR07606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
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                                                                                                                               standard;
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/label= T4/LFA-3/AD gene product
267. .295
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                                                                                                                             protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Phosphatidyl-inositol linkage signalling DNA sequence -
                                                                                                                                                                                                                                                                                                                               Sequence 318
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        plasmid T4/LFA-3/2 gene product with C-terminal encoding
phosphatidylinositol (PI) linkage signaling sequence.
            AAY39825;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Wallner
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Peptide
                                  AAY39825 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              10-APR-1989;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9012099-A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unidentified
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                                                                                                                                                                                                                                                1 MANGYPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                             Similarity
                                                                                          TWTCTVLQNQKKVEFKIDIVVLAFQKAS 208
                                                                                                                                                      LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                   | ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                         LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSV
                                                                                                                                                                                     ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                    MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                      field.)
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                                                                                                                                                                                                                                                                                39.9%;
ilarity 100.0%;
Conservative (
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/label=
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/label= LFA-3 gene product
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                                  protein;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
                                   394
                                                                                                                                                                                                                                                                                Score 1064; DB 2;
Pred. No. 6.9e-47;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       peptide
                                                                                                                                                                                                                                                                                                      Length 318;
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11-JUN-1991;
06-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents the soluble human T4 protein of the invention. The soluble human T4 protein blocks the binding of HIV to T4+ cells and is therefore useful for the treatment of AIDS. Monoclonal antibodies against the T4 protein may be used as vaccines for immunising subjects against AIDS
          sT4; glycoprotein; human immunodeficiency virus; HIV; block binding; AIDS; treatment; inhibit; cell to cell spread; infection; fusion.
                                          T4 glycoprotein amino acid sequence
                                                               14-JUL-2000
                                                                                                                                                                                                                                                                                                                                                                                  Sequence 394 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Col 13-16; 58pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human T4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              N-PSDB; AAZ20694
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mcdougal JS,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Soluble T4 vaccine; in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Soluble human
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                                                                                                          AAY88328 standard;
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                                                                                                                                                                                                                                                                                                         1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                   Similarity
                                                                                                                                                                                                      LVFGLTANSDTHILLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                              LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
                                                                                                                                                                                                                                                                ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein inhibits HIV binding to T4 cells, useful
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      If protein; sT4; human;
immunisation; therapy.
                                                                                                                                                                           TWTCTVLQNQKKVEFKIDIVVLAFQKAS 208
                                                                                                                                                                                                                                                   ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                              MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                TWICTVLONOKKVEFKIDIVVLAFOKAS
                                                                                                                                                                                                                                                                                                                                       39.9%; So ilarity 100.0%; I Conservative 0;
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91US-00713564.
92US-00909021.
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                                                               entry)
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                                                                                                          394
                                                                                                                                                                                                                                                                                                                                                Score 1064; DB 2;
Pred. No. 8.3e-47;
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RESULT 6
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KW CD4,
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents the full length amino acid sequence of glycosylated sT4 glycoprotein. Human immunodeficiency virus (HIV) uses ST4 as a target receptor on T cells. The invention relates to glycosylated sT4 which functions by blocking the binding of HIV to T4 target cells, and can be used for the prophylaxis and treatment of AIDS patients. Administration of sT4 effectively inhibits the cell to cell spreading of HIV infection and also the fusion of HIV-infected T4 cells and non-infected T4 cells. The administration of T4 alleviates several symptoms associated with AIDS, and prevents the occurrence of new pathological changes. The sT4 glycoprotein is useful as a reagent to identify natural, synthetic or recombinant molecules which act as the appentic agents or inhibitors of T4+ cell interactions and in
CD4; IgM; human; CD4Mmu; fusion protein; immunoglobulin; HIV; SIV; gp120; therapy; diagnosis.
                                              CD4-IgM fusion protein CH4Mmu.
                                                                                                                                          AAB19509 standard; protein; 416 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Soluble T4 glycoprotein useful for prevention and treatment of acquired immunodeficiency syndrome and for screening inhibitors of human immunodeficiency viral binding.
                                                                              09-JAN-2001
                                                                                                             AAB19509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 394
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diagnostic assays
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                                                                                                                                                                                                                      TWTCTVLQNQKKVEFKIDIVVLAFQKAS
                                                                                                                                                                                                                                                   TWTCTVLQNQKKVEFKIDIVVLAFQKAS 208
                                                                                                                                                                                                                                                                                 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                             ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                          MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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                                                                             (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             for detection T4 proteins or molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                      °,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1064; DB 3;
Pred. No. 8.3e-47;
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Best Local S
Matches 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      22-JAN-1988;
23-JAN-1989;
09-JUN-1992;
12-APR-1993;
                                                                                                                                                                                                                                                                                                         Sequence 416 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 1; Col 41-50; 39pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CD4-immunoglobulin fusion proteins, useful for targeting gp120 of HIV or
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                                                                                                                                                                                  1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GEN
                                                                                                                                                                                                                                                              Similarity
                                                                                                                                       ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                    MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQPHWKNSNQIK
                                                                           LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                       ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                 TWTCTVLQNQKKVEFKIDIVVLAFQKAS
TWTCTVLQNQKKVEFKIDIVVLAFQKAS 208
                                                           LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HOSPITAL CORP.
                                                                                                                                                                                                                                            39.9%; Score 1064; DB 3; ilarity 100.0%; Pred. No. 8.7e-47; Conservative 0; Mismatches 0;
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89US-00299596.
92US-00896781.
93US-00057952.
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400. .416
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                                                                                                                                                                                                                                                                         Length 416;
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RESULT 7
AAY51080
ID AAY51080 standard;

protein;

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RESULT 8
AAY88329
ID AAY8
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                          This invention describes a novel nucleic acid (I) encoding a fusion protein comprising a DNA sequence encoding amino acids 1-173 of CD4 (II) and a DNA sequence encoding a human immunoglobulin (Ig) heavy or light chain (III). The products pf the invention have anti-human immunodeficiency virus (HIV) activity and are capable of binding to gp120. The fusion protein is useful for treating human immunodeficiency virus (HIV) or simian immunodeficiency virus (SIV). This sequence represents the fusion protein CD4Mg which is constructed from CD4 linked to human IgM upstream of the CH1 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fusion protein; human; CD4; IgM; immunoglobulin; gp120; anti-human immunodeficiency virus; CD4Mg.
 AAY88329;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Col 41-50; 39pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Seed B;
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09-JUN-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Synthetic.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         23-MAR-2000
                           AAY88329
                                                                                                                                                                                                                                                                                                                                                    Sequence 436 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-JAN-1988;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Human fusion protein CD4Mg
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (GEHO)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   protein useful for the treatment of human immunodeficiency virus
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                                                                                                                                                                                                                                                                                                              Similarity
                                                                                                        TWTCTVLQNQKKVEFKIDIVVLAFQKAS
                                                                                                                                           LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                            LVFGLTANSDTHLLQGQSLTLITLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
                                                                                                                                                                                                            | ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                             MRRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKS1QFHWKNSNQIK
                                                                                                                                                                                                                                                            MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                         standard; protein; 458
                                                                                                                                                                                             ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                         TWTCTVLQNQKKVEFKIDIVVLAFQKAS 208
                                                                                                                                                                                                                                                                                                  Conservative
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89US-00299596.
92US-00896781.
93US-00057952.
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                                                                                                                                                                                                                                                                                                Score 1064; DB 3;
Pred. No. 9.1e-47;
0; Mismatches 0;
                                                                                                                208
                                                                                                                                                                                                                                                                                                                         Length 436;
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RESULT 9 AAB81502

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standard; protein; 458

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                                                                                                                                                                                                                            Matches 208;
                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                          This sequence represents the amino acid sequence of glycosylated sT4 glycoprotein. Human immunodeficiency virus (HIV) uses sT4 as a target receptor on T cells. The invention relates to glycosylated sT4 which functions by blocking the binding of HIV to T4 target cells, and can be used for the prophylaxis and treatment of AIDS patients. Administration of sT4 effectively inhibits the cell to cell spreading of HIV infection and also the fusion of HIV-infected T4 cells and non-infected T4 cells. The administration of T4 alleviates several symptoms associated with AIDS, and prevents the occurrence of new pathological changes. The sT4 glycoprotein is useful as a reagent to identify natural, synthetic or recombinant molecules which act as therapeutic agents or inhibitors of T4+ cell interactions and in diagnostic assays for detection T4 proteins
                                                                                                                                                                                                                                                                                     Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Soluble T4 glycoprotein useful for immunodeficiency syndrome and for immunodeficiency viral binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   sT4; glycoprotein; human immunodeficiency virus; HIV; block binding; AIDS; treatment; inhibit; cell to cell spread; infection; fusion.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             T4 glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example; Fig 6; 64pp; English
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                                                                                                                                                                                                                                           Local Similarity
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181
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                                                                                                                                         61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                                                                                                                                                                                                                                                                      458
                                                                      LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                            MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                     LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
TWTCTVLQNQKKVEFKIDIVVLAFQKAS 208
                TWTCTVLQNQKKVEFKIDIVVLAFQKAS 208
                                                                                                                                                                     MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                              Conservative
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                                                                                                                                                                                                                                                                                     AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COLUMBIA NEW YORK.
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                                                                                                                                                                                                                                          39.9%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Axel R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sequence.
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                                                                                                                                                                                                                                          Pred. No. 9.5e-47;
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                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         r prevention and treatment of acquired screening inhibitors of human
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The present sequence is human CD4. Human CD4 extracellular domains 1 and C2 were used in the construction of CD4 oligomerisation fusion proteins. The fusion proteins contain an oligomerisation domain that enables the proteins to bind to one another to form oligomers. The oligomers may be used in an invention relating to a method for screening for compounds with the ability to inhibit a low affinity receptor-ligand interaction. The method uses an interfacial optical assay, such as surface plasmon resonance (SPR). The method is useful for screening candidate compounds for the ability to inhibit interaction between MHC/peptide complex and TC cell receptor, and MHC/peptide complex and CDB or CD4 co-receptor. The compounds identified by the above methods which interfere with T cell receptor binding to a particular HLA type molecule are useful as immune inhibitors for treating carcinomas, autolammune diseases such as multiple sclerosis, human immunodeficiency virus (HIV) infection, rheumatoid carthritis, Hashimoto's disease, insulin dependent diabetes, Good pasture's syndrome, uveitis, psoriasis and graft rejection
                                                                                                                                                                                                                                                                                                                                                Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                        Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequential screening of candidate compounds library for those which inhibit binding of low affinity receptor-ligand interaction having binding kinetics, using interfacial optical assay.
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                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence
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LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                     ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                         ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                        Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                      AA;
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                                                                                                                                                                                                                                                                                                                                                39.9%;
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                                                                                                                                                                                                                                                                                                                     Score 1064; DB 4;
Pred. No. 9.5e-47;
0; Mismatches 0;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The specification describes an antibody which is specific for an antigenic fragment of gp120. This antigenic fragment binds to DC-SIGN or is exposed upon gp120 binding of DC-SIGN due to concomitant conformational change. DC-SIGN is a receptor that is specifically expressed on dendritic cells and facilitates infection of T lymphocytes with HIV. DC-SIGN is identical to a HIV-1 gp120-binding C-type lectin. It is specifically expressed constitutively on T lymphocytes with high affinity. The antibody of the invention inhibits the transenhancement of HIV entry into a T cell or macrophage facilitated by dendritic cells. The antibody is useful to treat or prevent HIV infection. The present sequence represents a human CD4 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         An antibody for the treatment or prevention of HIV-infection comprises gp120 portion which binds to DC-SIGN or is exposed upon gp120 binding c DC-SIGN due to concomitant conformational change.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 458 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Page 115-116; 131pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              C-type lectin;
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                                                                                                                                                     61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                              LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
                                                                                                                                                                                                                                                                      MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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                                                                                                                                                                                                                                 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                                                                                                                                                                                Score 1064; DB 4;
Pred. No. 9.5e-47;
                                                                                                                                                                                                                                                                                                                                                        Mismatches
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The invention relates to a binding domain-immunoglobulin fusion protein CC comprising a binding domain polypeptide, an immunoglobulin heavy chain CC immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain CC constant region polypeptide that is fused to the hinge region CC polypeptide, and an immunoglobulin heavy chain CH3 constant region CC polypeptide, and an immunoglobulin heavy chain CH3 constant region CC polypeptide, and an immunoglobulin heavy chain CH3 constant region CC polypeptide, a mutated human IgG1 immunoglobulin hinge region polypeptide, a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues, where the first cysteine is not mutated; a contains 2 cysteine residues, where the first cysteine is not mutated; a contains 2 cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide, derived from CC (a) having 3 or more cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no more than one cysteine residues; and a mutated human IgG1 immunoglobulin hinge region cysteine residues; where the mutated human IgG1 concretains no more than one cysteine residues; where the mutated human IgG1 immunoglobulin hinge region cysteine residues. The binding domain-immunoglobulin hinge region polypeptide contains no cysteine residues. The binding domain-immunoglobulin fusion protein is capable of at least one immunological activity comprising antibody companies of at least one immunological activity comprising antibody companies of the mutated cytotoxicity (ADCC) and complement fixation. The binding domain-immunoglobulin fusion protein is companies of specifically binding to an construct comprising the polymcleotide (operably linked to a promoter), construct comprising the polymcleotide (operably linked to a promoter), construct comprising the polymcleotide with a recombinant expression construct comprising the polymcleotide with a recombinant expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              17-JAN-2001; 2001US-0367358P
17-JAN-2002; 2002US-00053530
03-JUN-2002; 2002US-0385691P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma; rheumatoid arthritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Binding domain; immunoglobulin; fusion protein; cytostatic; antiarthritic; immunosuppressive; antidiabetic; antithyroid; neuroprotective; hinge region; immunoglobulin heavy chain; CH2 constant region; CH3 constant region; IgG1; antibody dependent cell-mediated cytotoxicity; ADCC; complement fixation;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Disclosure; SEQ ID NO 170; 157pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ledbetter JA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          15-JAN-2004
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                                                                                                                                                                                                                                                                   14-AUG-2001; 2001US-0312147P
01-NOV-2001; 2001US-0346382P
26-NOV-2001; 2001US-0333347P
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                            WPI; 2003-268312/26
GENBANK; P01730.
                                                                                                                     Woolf C,
                                                                                                                                                                                 (GEHO )
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segmental nerve injury; chronic cons
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BAYER AG.
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                                                                                                                  D'urso D,
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                                                                                                                     Befort K,
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CC claimed are a vector, a method for identifying a nucleotide, a host cell comprising the vector, a method for identifying a nucleotide sequence CC which is differentially regulated in an animal subjected to pain and a CC kit to perform the method, an array, a method for identifying an agent that increases or decreases the expression of the polynucleotide sequence CC that is differentially expressed in neuronal tissue of a first animal CC subjected to pain, a method for identifying an agent CC the expression of a polynucleotide sequence which is differentially expressed in an animal subjected to pain, a method for identifying a compound which regulates CC the expression of a polynucleotide sequence which is differentially CC expressed in an animal subjected to pain, a method for identifying a compound which regulates the cc compound that regulates the activity of one or more of the polynucleotides, a method for producing a pharmaceutical composition, a method for identifying a compound useful in treating compain and a pharmaceutical composition comprising the one or more complypeptides or their antibodies. The polynucleotide or the compound that cc polynucleotide or their antibodies. The polynucleotide or the compound that composition comprising a medicament for treating pain (e.g. spinal segmental nerve injury (CNINg), chronic constriction conjury (CCI) and spared nerve injury (SNI) in an animal (e.g. gene CC the specification) which is differentially expressed during pain. Note: CT has because data for this patent did not form part of the printed composition introduced at the printed in electronic form directly from WIPO at the confidence of the printed of the printed of the printed composition introduced in electronic form directly from WIPO at the specification, but was obtained in electronic form directly from WIPO at
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local (
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                           WO2004042346-A2
                                                                                                                                  transplant
                                                                                                                                                                           Protein encoded by mRNA of the invention #105.
                                                                                                                                                                                                                        12-AUG-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           derivative or allelic variation of the nucleic acid sequence. Also
                                                                   Ното варіелв
                                                                                                              inflammatory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  invention discloses a composition comprising two or more isolated rat
                                                                                                                                                                                                                                                                                                                                                                                                                        181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                      TWTCTVLQNQKKVEFKIDIVVLAFQKAS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                                                                                                                  rejection; immune system;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Conservative
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                                                                                                                                                                                                                      (first entry)
                                                                                                                bowel
                                                                                                                disease;
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                                                                                                              multiple
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                                                                                                            rheumatoid arthritis; lupus; sclerosis; HIV; AIDS.
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Best Local
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              HIV-1 infection; human immunodeficiency virus-1; CD4+ cell; chimeric endoplasmic reticulum; ER retention; envelope protein gp160; T cell receptor CD9epsilon chain; C-terminal domain; CD4epsilon15; gene therapy; human; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of
                                                                                                       CD4/TCR CD3epsilon chain chimeric protein CD4epsilon15,
                                                                                                                                          04-DEC-2003
                                                                                                                                                                                                              ADA44807 standard; protein; 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 458 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The present invention relates to diagnosing or monitoring transplant
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 65; SEQ ID NO 2504; 1762pp; English.
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20-DEC-2002; 2002US-00325899.
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                                                                                                                                                                                                                                                                                                                                                                                                            121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
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                                                                                                                                                                                                                                                                                                                                    TWTCTVLONOKKVEFKIDIVVLAFOKAS 208
                                                                                                                                                                                                                                                                                                                                                                                                                                               ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Conservative
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                                                                                                                                          entry)
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Pred. No. 9.5e-47;
                                                                                                                                                                                                                B
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                                                                                                                                                                                                                                                                                                                                  The invention relates to a composition for the treatment or prevention of CC comprises CD4+ cells that have been transduced with a vector that encodes CC a chimeric CD4 molecule which is capable of being retained in the CC endoplasmic reticulum (ER). The invention also encompasses the use of a Soluble protein factor produced by CD4+ cells that have been transduced CC with a vector encoding a chimeric CD4 protein; and the use of an CC expression system encoding a chimeric CD4 protein. The ER-localised CC chimeric CD4 molecule binds to the HIV-1 envelope protein gpi50, CC resulting in HIV-1 retention in the ER and thereby preventing viral CC comprises CD4 fused to 15 amino acids of the C-terminal domain of the TC cell receptor CD3epsilon chain; this chimeric CD4 molecule is designated CC CD4epsilon15 (ADA44807). A known chimeric CD4 of similar structure but CC containing only 10 amino acids from CD3epsilon can also be used. CC compositions of the invention have an in trans effect on the replication of HIV-1, and may be used to treat and prevent HIV-1 infection. The CC is specifically claimed for use in compositions of the invention.
                                                                                                                                                                                                                                                Matches
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Best Local
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Gomez Buendia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Claim 5; Page 33-35; 43pp; Spanish.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Composition for treating or preventing human immune deficiency virus, comprises CD4 chimeric protein having a protective effect in trans, or
                                                                                                                                                                                                                                                                                                           Sequence 473
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Chimeric
                                                                                                                                                                                                                                                              Local Similarity
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DB; ADA44806.
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mendia M;
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                                                                              LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
                                                                                                                                                                                                   MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                                            LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                     TWTCTVLQNQKKVEFKIDIVVLAFQKAS
                                                                                                                                                     ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
 TWTCTVLQNQKKVEFKIDIVVLAFQKAS
                                                                                                                                                                                                                                                Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note= "Part of the C-terminal domain of the T cell
receptor CD3epsilon chain"
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                                                                                                                                                                                                                                                             39.9%;
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AC CD4-I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention provides a fusion gene encoding a fusion protein that comprises an extracellular CD4 DNA sequence or its fragment which binds to HIV gp120 when fused to an immunoglobulin (Ig) chain and the DNA sequence of an Ig heavy or light chain, where the DNA sequence encoding the variable region has been replaced with the DNA sequence which encodes extracellular CD4 or its gp120 binding fragment. The fusion protein is capable of being secreted. The fusion proteins are useful for treating HIV or SIV infections in animals, preferably humans. They are also useful for producing medicaments which can be used for treating HIV or SIV infections. The present sequence represents the fusion protein in CD4Mmu where the CD4 is linked to human IgG1 at the Mst2 site upstream of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New fusion gene encoding immunoglobulin-CD4 fusion proteins, useful in the treatment of HIV or simian immunodeficiency virus infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Example 1; Page 47-53; 89pp; English
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         TWTCTVLQNQKKVEFKIDIVVLAFQKAS 208
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Pred. No. 9.8e-47;
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TWTCTVLQNQKKVEFKIDIVVLAFQKAS

Search completed: September 20, 2005, 16:07:08 Job time : 121 secs

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Perfect score:
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| 'cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
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| 'cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
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US-08-34-388A-29
US-08-34-311-1
US-08-34-57-408-1
US-08-34-57-408-1
US-08-34-57-408-1
US-08-328-500-9
US-08-467-368-4
US-08-318-5
US-08-284-391B-5
US-08-284-391B-5
US-08-384-391B-5
US-08-384-391B-6
US-08-284-391B-6
US-08-284-391B-6
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Sequence 29, Appl
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Sequence 4, Appli
Sequence 5, Appli
Sequence 6, Appli
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                                    RESULT 2
5223394-9
;Patent No. 5223394
; APPLICANT: WALLINER, BARBARA
; TITLE OF INVENTION: RECOMBINANT DNA MOLECULE COMPRISING
;LINKAGE SIGNAL SEQUENCE
;LINKAGE SIGNAL SEQUENCES; 12
; CURRENT APPLICATION DATA:
; CURRENT APPLICATION NUMBER: US,07/335,688
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121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG

LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG

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61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL

ILGNOGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL

1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK

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TWTCTVLQNQKKVEFKIDIVVLAFQKAS 208 TWTCTVLQNQKKVEFKIDIVVLAFQKAS

5223394-9

SEQ ID NO:9

LENGTH: 295

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RESULT 1

5223394-9
;Patent No. 5223394
; Patent No. 5223394
; APPLICANT: WALLNER, BARBARA
; TITLE OF INVENTION: RECOMBINANT DNA MOI
; LYMPHOCYTE FUNCTION-ASSOCIATED ANTIGEN 3 PH
;LINKAGE SIGNAL SEQUENCES: 12
; NUMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/335,688
                                     5223394-9
                                            FILING DATE: 10-APR-1989
SEQ ID NO:9:
LENGTH: 295
            Query Match
Best Local Similarity
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US-08-477-888A-6
5223394-7
US-08-477-460B-4
US-08-328-500-2
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US-08-328-500-2
US-08-328-500-4
US-08-38-77-460B-4
US-08-484-581-4
US-08-484-681-4
US-08-484-681-4
US-08-484-681-4
  Score 1064; DB 6;
; Pred. No. 9.1e-54;
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                  Length 295;
     Indels
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Patent No.
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Sequence 4
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9 8, Appli

9 9, Appli

9 1, Appli

9 4, Appli
     Gaps
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RESULT 3
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FPATENT NO. 5223394
APPLICANT: WALLNER, BARBARA
TITLE OF INVENTION: RECOMBINANT DNA MOLECULE COMPRISING
LYMPHOCYTE FUNCTION-ASSOCIATED ANTIGEN 3 PHOSPHATIDYLINOSITOL
LINKAGE SIGNAL SEQUENCE
                                                           ;PATERIT NO. 5223394
; APPLICANT: WALLNER, BARBARA
TITLE OF INVENTION: RECOMBINANT DNA MOLECULE COMPRISING;
LYMPHOCYTE FUNCTION-ASSOCIATED ANTIGEN 3 PHOSPHATIDYLINOSITOL;
LINKAGE SIGNAL SEQUENCE;
LUNGAGE OF SEQUENCES: 12
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/335,688
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CURRENT APPLICATION DATA:
APPLICATION NUMBER: US
                                FILING DATE: 10-APR-1989 NO:11:
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; MOLECULE TYPE:
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                                    Matches
                                                  Query Match
Best Local Similarity
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Best Local Similarity
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                                                                                                                                                                                                                                                                                          CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: DE 19710643.9
FILING DATE: 14-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 016779/0131
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Koerner, Kathrin
APPLICANT: Mueller, Rolf
APPLICANT: Sadlacek, Hans-Har
TITLE OF INVENTION: PREPARATI
TITLE OF INVENTION: PREPARATI
NUMBER OF SEQUENCES: 19
                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                               TELEPHONE: (202) 672-5399
                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: FILING DATE: 16-MAI
                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: D.C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Foley & Lardner STREET: 3000 K Street, N.W.,
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                                                  39.9%;
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100.0%; Pred. No. 9.8e-54;
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                                Score 1064; DB 3;
Pred. No. 1.4e-53;
0; Mismatches 0;
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                                                                   Length 458;
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; LENGTH: 458
; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-517-605-3
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US-09-517-605-3
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Sequence 25, Application US/10092138A

Patent No. 6743630

GENERAL INFORMATION:
APPLICANT: Sato, Taka-Aki
TITLE OF INVENTION: METHOD OF PREPARING A PROTEIN ARRAY BASED ON
TITLE OF INVENTION: BIOCHEMICAL PROTEIN-PROTEIN INTERACTION
FILE REFERENCE: 65823/JPM/PT
CURRENT APPLICATION NUMBER: US/10/092,138A
CURRENT FILLING DATE: 2002-03-06

NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CURRENT APPLICATION NUMBER: US/09/517,605
CURRENT FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 3
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APPLICANT: Littman, Dan R.
APPLICANT: Kwon, Douglas S.
APPLICANT: van Kooyk, Yvette
APPLICANT: Geijtenbeck, Theo
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
TITLE OF INVENTION: CELLS
ETLE REFERENCE: 1049-1-017
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 208; Conserv
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Patent No. 6391567
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.9%; Score 1064; DB 3; Length 458; ilarity 100.0%; Pred. No. 1.4e-53; Conservative 0; Mismatches 0; Indels
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US-08-284-391B-29
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast5EQ for Windows Version 2.
CURRENT APPLICATION DATA:
                                                                                                                                     CLASSIFICATION DATA:
CLASSIFICATION DATA:
PRIOR APPLICATION UNMBER: 08/195,395
APPLICATION NUMBER: 07/847,566
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: 1D1019, KAZEN 15,238
REGISTRATION NUMBER: 35,238
REGISTRATION NUMBER: 00786/2.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
      INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 398 amino acid
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APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/01 FILING DATE: 02-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: Boston
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les 207; Conservative
                                                                                                                    TELEFAX: 617-428-7045
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99.5%;
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Pred. No. 1.8e-53;
1; Mismatches 0
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RESULT 9
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APPLICANT: Seed, B.
APPLICANT: Banapou:
APPLICANT: Romeo, (
APPLICANT: KOlanus
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Patent No. 6284240
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches 207;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY: USA
ZIP: 02110
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/218,950
                                                                                                                                                                                CLASSIFICATION:
PRICR APPLICATION NUMBER: US/08/284,391
APPLICATION NUMBER: US/08/284,391
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
TELEX:
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                STRANDEDNESS: single TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: KOlanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
NUMBER OF SEQUENCES: 53
                                                                                  NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                     TELEPHONE:
                                                                                                                                                                                                                                                                                                                                                                         FILING DATE:
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                                                       : 617-428-0200
617-428-7045
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Banapour, Babak
Romeo, Charles
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99.5%;
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                                                                                                               00786/247001
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Pred. No. 2.3e-53;
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Patent No. 6753162
GENERAL INFORMATION:
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Best Local Similarity
Matches 207; Conser
                            APPLICATION NUMBER: 08/195,39
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,56
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,96
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTMARE: FastSEQ for Wind
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TOPOLOGY: lin
MOLECULE TYPE:
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APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
                                                                                                                                                                                                                                                                         APPLICATION NUMBER: UFILING DATE: 24-FEB-1
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                            SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 5
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FILING DATE: 02-AUG-1994
FILING DATE: 08/195,395
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STATE: MA
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                   TELEPHONE:
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6753162
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   USA
617-428-7045
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                                                                                                                                              07/665,961
                                                                                                                                                                                 07/847,566
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                                                                                                                                                                                                                                                            US/08/284,391
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Pred. No. 2.3e-53;
0; Mismatches 1,
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Matches
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SEQUENCE CHARACTERISTICS:
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/104329
FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
NAME: HABAK, JANET E. 28,616
REFERENCE/DOCKET NUMBER: 444P
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch,
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
NUMBER OF SEQUENCES: 25
                                                                                                                                                                               FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/250785
                                                                                                                                                                                                                                                                              FILING DATE: 02-MAY-1994
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                                                 OPERATING SYSTEM: PC-DOS/MS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
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nes 207; Conserv
                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/236,311
FILING DATE: 02-MAY-1994
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94080
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 California
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                                                                                                                                                                                                                                                                                                                                                                                                                                      E: 5.25 inch, 360 Kb floppy disk
IBM PC compatible
SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   39.7%;
                                                                                                                                                                                                                                             07/842777
                                                                                                                        07/104329
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                    444P1C2
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Patent No. 6117655
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INFORMATION FOR SEQ ID NO:
FILING DATE: 28-SEP-1988
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/104
FILING DATE: 02-CCT-1987
ATTORNEY/AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
LENGTH: 402 amino acid
                                                                                                   APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/250785
                                                                                                                                                      PRIOR APPLICATION DATA:
07/842777
                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: patin (Genentech) CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
                                                                                                                                                                                                                                  APPLICATION NUMBER: 08/236311
FILING DATE: 02-MAY-1994
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
                                                                                                                                                                                                  APPLICATION NUMBER: 07/936190 FILING DATE: 26-AUG-1992
                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/FILING DATE: 1-JUN-1995
CLASSIFICATION: 435
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207; Conserv
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                                                      07/104329
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Pred. No. 2.4e-53;
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Length 402; Indels

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RESULT 13
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TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
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GENERAL INFORMATION:
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Best Local Similarity
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TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                            CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/157,408
FILING DATE: 28-May-2002
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                  ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gregory, Timothy TITLE OF INVENTION: Adheson NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Capon, Daniel J.
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                                 APPLICATION NUMBER: US/08/457,918
FILING DATE: 1-JUN-1995
APPLICATION NUMBER: 08/236311
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: 07/942777
FILING DATE: 18-FEB-1992
APPLICATION NUMBER: 07/250785
FILING DATE: 18-FEB-1992
APPLICATION NUMBER: 07/250785
FILING DATE: 08-SEP-1988
APPLICATION NUMBER: 07/104329
FILING DATE: 02-CCT-1987
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                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
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CITY: South San Francisco
STATE: California
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                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: patin (Genentech)
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                    INFORMATION:
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Pred. No. 2.4e-53;
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Best Local (
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TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
TOPOLOGY: linear
              TELEFAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
LENGTH: 457 amino acids
                                                                                                                                     FILING DATE:
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575
                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/328,500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Maddon, Paul J.
APPLICANT: Axel, Richard
APPLICANT: Sweet, Richard W.
APPLICANT: Arthos, James
TITLE OF INVENTION: DERIVATIVES OF SOLUBLE
                                                                                               TELECOMMUNICATION INFORMATION: TELEPHONE: (212) 278-0400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: New York COUNTRY: U.S.A.
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REFERENCE/DOCKET NUMBER: PO-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
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Pred. No. 2.4e-53;
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RESULT 15
US-08-466-368-4
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                                                                                US-08-466-368-4
                                                                                                                                     REFERENCE/DOCKET NUMBER: 2457
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-278-0400
TELEPAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 4:
SEQUIENCE CHARACTERISTICS:
LENGTH: 458 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 4, Application US/08466368 Patent No. 6093539 GENERAL INFORMATION:
  Query Match 39.7%;
Best Local Similarity 99.5%;
Matches 207; Conservative
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Best Local S
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MEDIUM TYPE: Ploppy disk
COMPUTER: BM PC compatible
COMPUTER: COMPUTER: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Weiss, Robin
APPLICANT: McDougal, J. S.
TITLE OF INVENTION: DNA ENCODING THE T CELL SURFACE PROTEIN
TITLE OF INVENTION: T4 AND USE OF FRAGMENTS OF T4 IN THE TREATMENT OF AIDS
NUMBER OF SEQUENCES: 21
CORRESPONDENCE ADDRESS:
ADDRESSEE: Cooper & Dunham LLP
                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
                                                                                                  TOPOLOGY: li
                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/08/466,368 FILING DATE: 06-JUN-1995 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    / Match 39.7%;
Local Similarity 99.5%;
les 207; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STREET: 1185 Avenue of Americas CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  181 TWTCTVLQNQKKVEFKIDIVVLAFQKAS 208
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Littman, Dan R.
Chess, Leonard
Axel, Richard
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                                                                                                                       linear
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Score 1059; DB 3; Length 458; Pred. No. 2.7e-53; 0; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                24577-E1-B/JPW/AKC
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                    181 TWTCTVLQNQKKVEFKIDIVVLAFQKAS 208
                                                                                        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                    121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                                                                                                                                                                                                1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                  | ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPL1|KNLKIEDSDTYICEVEDQKEEVQL
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TWTCTVLQNQKKVEFKIDIVVLAFQKAS 208
                                                                                                                                        ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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Search completed: September 20, 2005, 16:10:48 Job time : 34 secs

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Minimum DB seq length: 0
Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Searched:
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Listing first 45 summaries
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Copyright
/ Cgn2 6/ptodata/1/pubpaa/US09A PUBCOMB.pep: *
/ Cgn2 6/ptodata/1/pubpaa/US09B PUBCOMB.pep: *
/ Cgn2 6/ptodata/1/pubpaa/US09B PUBCOMB.pep: *
/ Cgn2 6/ptodata/1/pubpaa/US090 NEW PUB.pep: *
/ Cgn2 6/ptodata/1/pubpaa/US10A PUBCOMB.pep: *
/ Cgn2 6/ptodata/1/pubpaa/US10A PUBCOMB.pep: *
/ Cgn2 6/ptodata/1/pubpaa/US10D PUBCOMB.pep: *
/ Cgn2 6/ptodata/1/pubpaa/US10D PUBCOMB.pep: *
/ Cgn2 6/ptodata/1/pubpaa/US10D PUBCOMB.pep: *
/ Cgn2 6/ptodata/1/pubpaa/US10 NEW PUB.pep: *
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/cgn2_6/ptodata/1/pubpaa/ECT_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_REW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US06_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US07_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/JC07US_PUBCOMB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
/cgn2_6/ptodata/1/pubpaa/US08_NEW_PUB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

11	10	9	80	7	σ	5	4	ω	2	-	Result No.
1059	1059	1059	1062	1062	1062	1062	1064	1064	1064	1064	Score
39.7	39.7	39.7	39.8	39.8	39.8	39.8	39.9	39.9	39.9	39.9	Query Match
402	402	398	458	458	458	458	458	458	458	458	Query Match Length DB
14	14	10	16	14	10	8	14	14	14	14	DB
US-10-097-044A-1	US-10-157-408-1	US-09-939-537-29	US-10-820-403-25	US-10-092-138-25	US-09-230-111C-25	US-08-681-219-27	US-10-207-655-170	US-10-188-444-39	US-10-103-597A-39	US-10-151-274-3	ID
Sequence 1, Appli	Sequence 1, Appli	Sequence 29, Appl	Sequence 25, Appl	Sequence 25, Appl	Sequence 25, Appl	Sequence 27, Appl	Sequence 170, App	Sequence 39, Appl	Sequence 39, Appl	Sequence 3, Appli	Description

45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13	1
940	940	945.5	946	946	946	954	954	957.5	957.5	59.	959.5	1035	1036	1040	1040	1040	1040	1040	1048	1048	1050	1050	1051	1051	1053	1059	1059	1059	1059	1059	1059	1059	FOOT
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433	370	448	434	434	434	251	251	246	246	250	250	203	202	487	450	449	203	203	310	310	432	432	530	530	397	575	575	532	532	462	462	457	400
17	9	14	16	14	14	15	10	15	10	15	10	10	16	18	16	16	18	18	ø	α	9	œ	9	œ	H	11	10	11	10	11	10	11	6
US-10-872-198-129	US-09-759-841-6	US-10-024-329-32	US-10-769-247-4	-10	-10	US-10-293-418-1238	-09-880-748-	US-10-293-418-1268	-09-880-	US-10-293-418-1952	US-09-880-748-1952		-10-492-729-	-10-512-966-	-10-493-676-		10-512-966-	US-10-513-725-10	US-09-766-995-6	US-08-485-163-7	US-09-766-995-2	US-08-485-163-3	-09-766-99	US-08-485-163-5	-09-	US-09-243-008-4	-09-939-5	-09-243-0	-09-939-5	-09-243-	'n	-891-1	00-10-103-641-T
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ALIGNMENTS

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Sequence 3, Application US/10151274

Publication No. US20030064071A1

GENERAL INFORMATION:
APPLICANT: Littman, Dan R.
APPLICANT: Kwon, Douglas S.
APPLICANT: Van Kooyk, Yvette
APPLICANT: Geijtenbeck, Theo
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY
TITLE OF INVENTION: CELLS
FILE REFERENCE: 1049-1-017
CURRENT APPLICATION NUMBER: US/10/151,274
CURRENT APPLICATION NUMBER: US/09/517,605
PRIOR APPLICATION NUMBER: US/09/517,605
PRIOR APPLICATION NUMBER: US/09/517,605
PRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
LENGTH: 458
TYPE: PRI
ORGANISM: Homo sapiens
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                                                                                                                                                      Query Match 39.9%; Score 1064; DB 14; Best Local Similarity 100.0%; Pred. No. 7.4e-51; Matches 208; Conservative 0; Mismatches 0;
61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                                              1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                                     MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                            Indels
                                                                                                                                                                                                            Length 458;
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Indels Length

0,

Gaps

120

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Sequence 39, Application US/10188444
Publication No. US20030104635A1
GENERAL INFORMATION:
APPLICAMY: Jakobsen, Bent Karsten
TITLE OF INVENTION: Screening Methods
FILE REFERENCE: 102286.142 (CIP)
CURRENT APPLICATION UMBER: US/10/188,444
CURRENT FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: PCT/GB00/03579
PRIOR TILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: GB 9922352.1
PRIOR APPLICATION NUMBER: GB 9922352.1
PRIOR APPLICATION NUMBER: GB 9922352.1
PRIOR FILING DATE: 1999-09-21
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Homo sapiens US-10-103-597A-39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Jakobsen, Bent Karsten
TITLE OF INVENTION: Screening Methods
FILE REFERENCE: 102286.142
CURRENT APPLICATION NUMBER: US/10/103,597A
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: PCT/GB00/03579
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: GB 9922352.1
PRIOR FILING DATE: 1999-09-21
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-103-597A-39
                 NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local (
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Publication No.
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  LENGTH:
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No. US20030096432A1
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Publication No. US20030118592A1

GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 39069.401C1

CURRENT APPLICATION NUMBER: US/10/207,655

CURRENT FILING DATE: 2002-07-25

NUMBER OF SEQ ID NOS: 426

SOFTWARE: Patentin version 3.0

SEQ ID NO 170
LENGTH: 458
TYDE: PRT
ORGANISM: Homo sapiens
US-10-207-655-170
                                                US-08-681-219-27
; Sequence 27, Application US/08681219
; Publication No. US20020058607A1
; GENERAL INFORMATION:
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Best Local Similarity
Matches 208; Conserv
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Best Local Similarity
APPLICANT: Takaaki Sato and Junn Yanagisawa
TITLE OF INVENTION: COMPOUNDS THAT INHIBIT THE INTERACTION BETWEEN
TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF
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100.0%; Pred. No. 7.4e-51;
vative 0; Mismatches 0;
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Length 458; Indels

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Gaps

120

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; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-08-681-219-27
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NAME: White, John P

REGISTRATION NUMBER: 28,678

REFERENCE/DOCKET NUMBER: 0575

TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPAX: (212) 278-0400
TELEPAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
                                           Sequence 25, Application US/09230111C
Publication No. US20030203414A1
GENERAL INFORMATION:
APPLICANT: Sato, Taka-Aki
APPLICANT: Yanagisawa, Junn
TITLE OF INVENTION: COMPOUNDS THAT INHIBIT INTERACTION BETWEEN
TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF (PDZ/DHR)
TITLE OF INVENTION: DOMAIN AND USES THEREOF
FILE REFERENCE: 48962-A-PCT-US
CURRENT APPLICATION UMBER: US/09/230,111C
CURRENT FILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 33
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Best Local (
SEQ ID NO 25
LENGTH: 458
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                              SOFTWARE: PatentIn Ver.
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CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
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NUMBER OF SEQUENCES:
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STRANDEDNESS: single
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CLASSIFICATION: 435
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Local Similarity 99.5%;
les 207; Conservative
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1185 Avenue of the Americas
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Pred. No. 9.5e-51;
1; Mismatches 0
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US-09-230-111C-25
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US-10-092-138-25
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                                                                                                                        RESULT 8
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APPLICANT: Sato, Taka-Aki
APPLICANT: Sato, Taka-Aki
TITLE OF INVENTION: METHOD OF PREPARING A PROTEIN ARRAY BASED ON
FILE REFERENCE: 65823/JPW/PT
CURRENT APPLICATION NUMBER: US/10/092,138
CURRENT FILING DATE: 2002-09-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 25
LENGTH: 458
TYPE: PRT
ORGANISM: human
US-10-092-138-25
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Publication No. US20030170723A1
GENERAL INFORMATION:
Sequence 25, Application US/10820403
Publication No. US20040229287A1
GENERAL INFORMATION:
APPLICANT: Sato, Taka-Aki
TITLE OF INVENTION: BITCHEMICAL PROTEIN ARRAY BASED ON
TITLE OF INVENTION: BITCHEMICAL PROTEIN-PROTEIN INTERACTION
FILE REFERENCE: 65823/JPW/PT
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Matches 207; Conservative
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    Mismatches

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Pred. No. 9.5e-51;
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LENGTH: 458
; TYPE: PRT
; ORGANISM: human
US-10-820-403-25
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Publication No. US2003
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CURRENT APPLICATION NUMBER: US/10/820,403
CURRENT FILING DATE: 2004-04-08
PRIOR APPLICATION NUMBER: US/10/092,138
PRIOR FILING DATE: 2002-03-06
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver: 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                                 OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,537
FILING DATE: 24-Aug-2001
CLASSIFICATION: <UNKnown>
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35
                                                                                                                                                                                                                                                                                                                                                         ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Banapour, Babak
Romeo, Charles
Romeo, Charles
Rolanus, Waldemar
TITLE OP INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Seed, Brian
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                                                    APPLICATION NUMBER: 08/284,391
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
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99.5%;
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1; Mismatches 0
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RESULT 10
US-10-157-408-1
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
                                                                                                     SOFTWARE: patin (Genentech)

CURRENT APPLICATION UNMBER: US/10/157,408

PILING DATE: 28-May-2002

CLASSIFICATION 1435

PRIOR APPLICATION UNMBER: US/08/457,918

APPLICATION NUMBER: US/08/457,918

FILING DATE: 1-JUN-1995

APPLICATION NUMBER: 08/236311

FILING DATE: 02-MAY-1994

APPLICATION NUMBER: 07/936190

ETITING DATE: 07/936190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch,
COMPUTER: IBM PC compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 29:
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TELEPAX: 617-428-7045
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STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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TYPE: amino acid
STRANDEDNESS: single
FILING DATE:
APPLICATION
                                   APPLICATION NUMBER: 07/250785
                                                        FILING DATE: 18-FEB-1992
                                                                      FILING DATE: 26-AUG-1992
APPLICATION NUMBER: 07/842777
                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 94080
                                                                                                                                                                                                                                                                                                                                                                                                                COUNTRY: USA
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compatible
M: PC-DOS/MS-DOS
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Pred. No. 1.2e-50;
""matches 1;
07/104329
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                                                                                                                                                                                                                                                                                                                                                       floppy disk
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RESULT 11
US-10-097-044A-1
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Best Local Similarity
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
                                                                                                                                                                                                                   COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/097,044A
FILING DATE: 28-May-2002
CLASSIFICATION: «Unknown»
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: amino acid
TOPOLOGY: linear
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0444P1C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/457,918
FILING DATE: 1-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 94080
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gregory, Timothy J. TITLE OF INVENTION: Adheson Variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Capon, Daniel J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181 TWTCTVLQNQKKVEFKIDIVVLAFQKAS 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: California
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TELEFAX: 415/952-9881
                                                         APPLICATION NUMBER: 08/236311
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
                                                                                                                                                                                                                                                                                                                                                                         MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
                  APPLICATION NUMBER: 07/842777 FILING DATE: 18-FEB-1992
APPLICATION
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NUMBER: 07/250785
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Pred. No. 1.2e-50;
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US-10-769-247-1
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Publication No. US20040197809A1
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
                                                         SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/10/769,247
FILING DATE: 30-Jan-2004
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/457,918
FILING DATE: 1-UN-1995
APPLICATION NUMBER: 08/236311
FILING DATE: 02-MAY-1994
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ATTORNEY AGENT INFORMATION:
NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0444P1C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                             ZIP: 94080
COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gregory, Timothy J. TITLE OF INVENTION: Adheson Variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Capon, Daniel J.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: 460 Point San Bruno
CITY: South San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TWTCTVLQNQKKVEFKIDIVVLAFQKAS 208
                    APPLICATION NUMBER: 07/936190 FILING DATE: 26-AUG-1992
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TELEFAX: 415/952-9881
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APPLICATION NUMBER: 07/104329
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 402 amino acids
  APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  39.7%;
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Pred. No. 1.2e-50;
0; Mismatches 1
  07/842777
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; LENGTH: 457
; TYPE: PRT
; ORGANISM: human
US-09-891-119A-9
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Publication No. US20040013683A1
GENERAL INFORMATION:
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: DERINATIVES OF SOLUBLE T-4
FILLE REFERENCE: 2457-CY-B
CURRENT APPLICATION NUMBER: US/09/891,119A
CURRENT FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
SEQ ID NO 9
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                                                                                                                                                                                              Query Match 39.7%;
Best Local Similarity 99.5%;
Matches 207; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino acids
TYPE: amino acid
TOPOLOGY: linear
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APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1998
APPLICATION NUMBER: 07/104329
FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
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REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0444P1C3
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
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121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
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                                                               61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
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                                                                                                                                         1 MNRGVPFRHILLIVIQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                                                                                                     1 MNRGVPFRHLLLVLQLÄLLPÄÄTQGNKVVLGKKGDTVELTCTÄSQKKSIQFHWKNSNQIK 60
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                                       ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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99.5%;
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                                                                                                                                                                                                                   Score 1059; DB 11
Pred. No. 1.4e-50;
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                                                                                                                                                                                                   Mismatches
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US-09-939-537-5
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Matches
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Publication No. US20030138410A1
GENERAL INFORMATION:
                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                            TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION UNMBER: 08/284,391
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                          Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: FastSEQ for Windows Veri
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/939,537
FILING DATE: 24-Aug-2001
CLASSIFICATION: CUNknown>
                                                                                                                                                                                                                                        MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
CELLS BY CHIMERIC CD4 RECEPTOR- BEJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Seed, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                                                                                                          l Similarity
207; Conser
                                                             1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                                                                      1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
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OPERATING SYSTEM: DOS
SOFTWARE: FASTSEO for Windows Version 2.0
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                                                                                                                                                                                                                                                                               TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
                                                                                                                                                                                                                                                                                                                       TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                         LENGTH: 462 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                     TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COUNTRY: USA
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                                                                                                                                            Conservative
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Romeo, Charles
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                                                                                                                                       Score 1059; DB 10;
Pred. No. 1.4e-50;
0; Mismatches 1;
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                                                                                                                                                                               Length 462;
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RESULT 15
US-09-243-008-5
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APPLICANT: Seed, Brian et al.
                                                                                                                                                                                                                                                                              Query Match 39.7%;
Best Local Similarity 99.5%;
Matches 207; Conservative
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 462 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READBALE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 553X
COMPUTER: WORLD THE TOTAL THE 
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: proteain
SEQUENCE DESCRIPTION: SEQ ID NO: 5:
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Receptor Chimeras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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61
                                                                                                                                   STREET: 225 Franklin Street CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                                                                                                                                                                                                                                                              Score 1059; DB 11; Length 462; Pred. No. 1.4e-50; 0; Mismatches 1; Indels 0
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        Qy
        121 LVFGLTANSDTHLLQGOSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
        180

        Db
        121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
        180

        Qy
        181 TWTCTVLQNQKKVEFKIDIVVLAFQKAS
        208

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        181 TWTCTVLQNQKKVEFKIDIVVLAFQKAS
        208

        Db
        181 TWTCTVLQNQKKVEFKIDIVVLAFQKAS
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Search completed: September 20, 2005, 16:27:40 Job time : 487 secs

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Result
No.
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Maximum Match 100%
Listing first 45 s
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Maximum DB seq length: 2000000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Scoring table:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence:
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Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OM protein - protein search, using sw model
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        Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
        Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PIR 79:*
1: pir1:*
2: pir2:*
3: pir3:*
4: pir4:*
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Match
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Gapop 10.0 , Gapext 0.5
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2668
1 MNRGVPFRHLLLVLQLALLP.....GTRLEIKLVPRGSGHHHHHH 508
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                                           231.1
225.0
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Length
      DB
    RWHUT4
RWCT4
RWCT4
RWCT4
RWCT4
RWCT4
RA5324
S31932
S31932
RWMST4
RWST4
RWWGT4
RWST4

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T-cell surface gly
T-cell surface gly
T-cell surface gly
I heavy chain V r
single chain Fv an
CD4 precursor - ra
a p53 specific singl
T-cell surface gly
I cell surface gly
I skappa chain V r
I skappa chain V r
I skappa chain V-I
I skappa chain V r
I skappa chain V-I
I skappa chain pre
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4 5	44	43	42	41	40	39	38	37	36	ა 5	34	ω u	32	31	30
436.5	437.5	438	438.5	438.5	440.5	440.5	441.5	441.5	443.5	445.5	448	448.5	449	451	451
16.4	16.4	16.4	16.4	16.4	16.5	16.5	16.5	16.5	16.6	16.7	16.8	16.8	16.8	16.9	16.9
109	109	107	109	109	109	107	134	129	108	627	128	109	110	215	95
N	N	N	N	N	N	N	N	N	N	N	N	N	N	N	N
G30601	B30601	S57444	F30607	A30608	PH0963	PH0965	S38643	S46369	C30608	S14683	\$40379	H30601	S40326	JE0243	PH0868
kappa	kappa	kappa	kappa	kappa		kappa	kappa		Ig kappa ch	Ig mu chain	kappa	Ig kappa ch	r kappa	Ig kappa ch	Ig kappa ch
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V-I	V-1	V-J	V-I	V-I	۷r	٧٢	۷r	var	V-I	ecur	V-J	V-I	V-J	NIG	Vr

ALIGNMENTS

A; Molecule type: mkNA A; Residues: 26-426,428-458 <cam> A; Residues: 26-426,428-458 <cam> A; Residues: 26-426,428-458, Folena-Wasserman, G.; Sweet, R.W.; Anumula, K.; Barr, J.R.; J. Biol. Chem. 264, 21286-21295, 1989 A; Title: Protein and carbohydrate structural analysis of a recombinant soluble CD4 recept A; Reference number: A34194; MUID:90078233; PMID:2592374 A; Contents: disulfide bonds; carbohydrate-binding sites A; Accession: A34194 A; Molecule type: protein A; Residues: 26-394 <car> R; Lederman, S.; DeMartino, J.A.; Daugherty, B.L.; Foeldvari, I.; Yellin, M.J.; Cleary, A. Mol. Immunol. 28, 1171-1181, 1991 A; Title: A single amino acid substitution in a common African allele of the CD4 molecule A; Accession: A53287 A; Stratus: not compared with conceptual translation</car></cam></cam>	A; Recession: A90872 A; Accession: A90872 A; Molecule type: mRNA A; Residues: 1-25, 'N', 27-458 < MAD> A; Residues: 1-25, 'N', 27-458 < MAD> A; Cross-references: UNIPROT: P01730 A; Experimental source: clone pT4B R; Littman, D.R.; Maddon, P.J.; Axel, R. Cell 55, 541, 1988 A; Title: Corrected CD4 sequence. A; Reference number: A90907; MUID:89028665; PMID:3263213 A; Contents: annotation; revision to residue 26 R; Camerini, D.; Seed, B. Cell 60, 747-754, 1990 A; Title: A CD4 domain important for HIV-mediated syncytium formation lies outside the via A; Title: A CD4 domain important for HIV-mediated syncytium formation lies outside the via A; Reference number: A32722; MUID:90182664; PMID:2107024 A; Accession: A32722 A; Status: nucleic acid sequence not shown; not compared with conceptual translation	RESULT 1 RWHUT4 RWHUT4 RWHUT4 T-cell surface glycoprotein CD4 precursor [validated] - human T-cell surface glycoprotein CD4 precursor [validated] - human N;Alternate names: T-cell surface antigen T4/Leu 3 C;Species: Homo sapiens (man) C;Date: 28-May-1986 #sequence revision 31-Dec-1988 #text change 09-Jul-2004 C;Accession: A90872; A32722; A34194; A53287; I54176; I54297; A02109; A30039 C;Accession: A90872; A32722; A34194; A53287; Maddon, D.E.; Chess, L.; Axel, R. R;Maddon, P.J.; Littman, D.R.; Godfrey, M.; Maddon, D.E.; Chess, L.; Axel, R. Cell 42, 93-104, 1985 A;Title: The isolation and nucleotide sequence of a cDNA encoding the T cell surface prot A, Deference and processors and processors and processors and processors and processors are processors and processor

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A;Gene: GDB:CD4
A;Map position: 12pter-12p12
A;Introns: 16/3
C;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology
C;Keywords: AID5; duplication; glycoprotein; T-cell; transmembrane protein
F;1-25/Domain: signal sequence #status predicted <SIG>
F;26-458/Product: T-cell surface glycoprotein CD4 #status experimental <MAT>
F;34-111/Domain: immunoglobulin homology <IM1>
F;136-299/Domain: immunoglobulin homology *IM3>
F;216-299/Domain: immunoglobulin homology <IM3>
F;211-372/Domain: immunoglobulin homology <IM3>
F;327-372/Domain: immunoglobulin homology <IM4>
F;397-420/Domain: inmunoglobulin homology <IM4
F;397-420/Do
                                                    N;Alternate names: T-cell surface antigen T4/Leu 3
C;Species: Pan troglodytes (chimpanzee)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: B3772; A46534
R;Camerini, D.; Seed, B.
Cell 60, 747-754, 1990
A;Title: A CD4 domain important for HIV-mediated syncytium formation lies outside the vi A;Accession: B3772
A;Mclecule: 1 CD4 domain important for HIV-mediated syncytium formation lies outside the vi A;Accession: B3772
A;Mclecule: CD4 domain important for HIV-mediated syncytium formation lies outside the vi A;Accession: B3772
A;Mclecule: A32722; MUID:90182664; PMID:2107024
A;Accession: B3772
A;Mclecule type: mRNA
A;Residues: 1-432 <CAM-
A;Residues: 1-432 <CAM-
A;Cross-references: UNIPROT:P16004; GB:M31135
R;Fomsgaard, A.; Hirsch, V.M.; Johnson, P.R.
Eur. J. Immunol. 22, 2973-2981, 1992
A;Title: Cloning and sequences of primate CD4 molecules: diversity of the cellular recep A;Title: Cloning and sequences of primate CD4 molecules: diversity of the cellular recep A;Title: Cloning and sequences of primate CD4 molecules: diversity of the cellular recep
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A;Cross-references: GB:M35160; NID:g179143; PIDN:AAA16069.1; PID:g179144
C;Comment: Macrophage tropic strains of HIV-1 bind to a complex of chemokine (C-C) recept
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A,Status: translated from GB/EMBL/DDBJ
A,Molecule type: DNA
A,Residues: 1-264,'W',266-458 <RE2>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              T-cell surface glycoprotein CD4 - chimpanzee N;Alternate names: T-cell surface antigen T4/Leu
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A; Status: not
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A; Residues: 1-72 < RES>
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Best Local :
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    compared with
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conceptual translation
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Pred. No. 1e-48;
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C:Comment: This protein is expressed on most thymocytes, on a subset of mature T-cells C:Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology C:Keywords: duplication; glycoprotein; T-cell; transmembrane protein F:1-432/product: T-cell surface glycoprotein CD4 #status predicted <MAT>
F:1-371/Domain: extracellular #status predicted <EXT>
F:9-86/Domain: immunoglobulin homology <IM1>
F:11-161/Domain: immunoglobulin homology #status atypical <IM2>
F:180-293/Domain: immunoglobulin homology <IM3>
F:296-347/Domain: immunoglobulin homology <IM4>
F:372-395/Domain: intransmembrane #status predicted <TMM>
F:372-395/Domain: intransmembrane #status predicted <INT>
F:16-84,30-159,303-345/Disulfide bonds: #status predicted
F:271,300/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A;Residues: 3-399 <FOM>
A;Residues: This protein is expressed on most thymocytes, on a subset of mature T-cells t?
C;Comment: This protein is expressed on most thymocytes, on a subset of mature T-cells t?
C;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology
C;Keywords: duplication; glycoprotein; T-cell; transmembrane protein
F;1-432/Product: T-cell surface glycoprotein CD4 #status predicted <MAT>
F;1-432/Product: T-cell surface glycoprotein CD4 #status predicted <MAT>
F;1-87/Domain: extracellular #status predicted <EXT>
F;9-86/Domain: immunoglobulin homology <IM1>
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F;191-274/Domain: immunoglobulin homology <IM3>
F;191-374/Domain: immunoglobulin homology <IM4>
F;296-347/Domain: immunoglobulin homology <IM4>
F;372-395/Domain: transmembrane #status predicted <TMM>
F;372-395/Domain: intracellular #status predicted <INT>
F;396-432/Domain: intracellular #status predicted <INT>
F;16-84,130-159,303-345/Disulfide bonds: #status predicted
F;271,300/Binding site: carbohydrate (Asn) (covalent) #status predicted
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A; Residues: 1-432 < CAM>
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R;Camerini, D.; Seed, B.
Cell 60, 747-754, 1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       T-cell surface glycoprotein CD4 - rhesus n
N;Alternate names: T-cell surface antigen
C;Species: Macaca mulatta (rhesus macaque)
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C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
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97.8%;
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                                                                                                  Score 831; DB 1;
Pred. No. 1.3e-36;
2; Mismatches 10
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antigen T4/Leu
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Pred. No. 4.9e-41;
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single chain Fv antibody - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 06-;
C;Accession: $41374
R;Artsaenko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.
submitted to the EMBL Data Library, January 1994
A;Description: Construction and functional characterization of a sin A;Reference number: $41374
A;Reference number: $41374
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-249 <ART>
A;Cross-references: EMBL:Z29480
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(;Species: Mus musculus (house mouse)
(;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change 16-Aug-1996
(;Accession: A56446
R;Tang, P.M.; Foltz, L.A.; Mahoney, W.C.; Schueler, P.A.
J. Biol. Chem. 270, 7829-7835, 1995
A;Title: A high affinity digoxin-binding protein displayed on M13 is functionally a high affinity digoxin-binding protein displayed on M13 is functionally a high affinity digoxin-binding protein displayed on M13 is functionally a high affinity digoxin-binding protein displayed on M13 is functionally a high affinity digoxin-binding protein displayed on M13 is functionally a high affinity digoxin-binding protein displayed on M13 is functionally a high affinity and the manual displayed on M13 is functionally a high affinity and the manual displayed on M13 is functionally a high affinity and the manual displayed on M13 is functionally a high affinity and the manual displayed on M13 is functionally a high affinity displayed on M13 is functionally and high affinity displayed on M13 is functionally a high affinity displaye
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C;Keywords: heterotetramer;
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Pred. No. 1.4e-32;
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C;Accession: JC5322
R;Jannot, C.B.; Hynes,
Biochem. Biophys. Res.
                                             p53 specific single-chain antibody Pab
C;Species: Homo sapiens (man)
C;Date: 15-May-1997 #sequence_revision
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 1-459 <HNG>
A;Residues: 1-459 <HNG>
A;Cross-references: UNIPROT:P46630; GB:M92840; NID:g164871; PIDN:AAA31198.1;
A;Cross-references: UNIPROT:P46630; GB:M92840; NID:g164871; PIDN:AAA31198.1;
A;Note: sequence extracted from NCBI backbone (NCBIN:112732, NCBIP:112733)
C;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology
F;322-372/Domain: immunoglobulin homology <IVM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Hague, B.F.; Sawasdikosol, S.; Brown, T.J.; Lee, K.; Recker, D.P.; proc. Natl. Acad. Sci. U.S.A. 89, 7963-7967, 1992
A;Title: CD4 and its role in infection of rabbit cell lines by human A;Reference number: A46254; MUID:92390370; PMID:1518821
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A46254
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Date: 21-Sep-1993 #sequence_revision 18-Nov-1994 #text_change 09-Jul-2004
Accession: A46254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                   ILGNOG----SFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKE 116
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                                                                                                                                                                                                           QDSGTWTCTV-LONOKKVEFKIDIVVLAFQKAS 208
                                                                                                                                                                                                                                              EVELLVFRLTANPNTRLLHGQSLTLTLEGPSVGSPSVQWKSPENKIIETGPTCSMPKLRL
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Pred. No. 1.7e-25;
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Pred. No. 2.5e-28;
                                                                                      Pab421
242-246,
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                                                   15-May-1997
                                                                                      human
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RESULT 8

$30.193
T-cell surface glycoprotein CD4 - dog
C:Species: Canis lupus familiaris (dog)
C:Species: Canis lupus familiaris (dog)
C:Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change 21-:
C:Accession: $30.193
C:Milde, K.F.; Conner, G.E.; Mintz, D.H.; Alejandro, R.
Biochim. Biophys. Acta 1172, 315-318, 1993
A:Title: Primary structure of the canine CD4 antigen.
A:Reference number: $30.193; MUID:93192324; PMID:7916632
A:Accession: $30.193
A:Status: preliminary
A:Rosidues: 1-422 cMIL-
A:Rosid
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A;Residues: 1-233 <JAN>
A;Experimental source: hydricloma cell
C;Comment: This protein specifically binds the tumor suppressor protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Cross-references: EMBL:X68565; NID:g288652; PIDN:CAB37664.1; PID:g4467377 (;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology C;Keywords: glycoprotein C;Keywords: glycoprotein F;202-311/Domain: immunoglobulin homology <IMM>
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Best Local 9
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                                                                              TCTVLQNQKKVEFKIDIVVLAFQKAS
                                                                                                                                                               GSSSGSSNIRLLQGQQLTLTLENPSGSSPSVQWKGPGNKSKHGGQNLSLSWPELQDGGTW
                                                                                                                                                                                                                                                                                                                                                                          LVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTK 71
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                                                       TCIISQSQKTVEFNINVLVLAFQKVS
                                                                                                                                                                                          ----NSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTW
                                                                                                                                                                                                                                                                      GSSRLKHRVESKKNLWDQGSFPLVIKDLEVADSGIYFCDT-DKRQEVELLVFNLTAKWDS
                                                                                                                                                                                                                                                                                                                     GPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTA----
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Pred. No. 1.2e-25;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 596; DB 2; ]
Pred. No. 2.4e-24;
8; Mismatches 42;
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RESULT 9
A27449
T-cell surface glycoprotein CD4 precursor - rat
N;Alternate names: W3/25 antigen
C;Species: Rattus norvegicus (Norway rat)
C;Species: Rattus norvegicus (Norway rat)
C;Accession: A27449; A33433
C;Accession: A27449; A33433
R;Clark, S.J.; Jefferies, W.A.; Barclay, A.N.; Gagnon, J.; Williams, A.F.
Proc. Natl. Acad. Sci. U.S.A. 84, 1649-1653, 1987
A,Title: Peptide and nucleotide sequences of rat CD4 (W3/25) antigen: evide:
A,Reference number: A27449; MUID:87175535; PMID:3104900
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:P05540; GB:M15768; NID:g203387; PIDN:AAA40901.1; PID:g203388 R;Davis, S.J.; Ward, H.A.; Puklavec, M.J.; Willis, A.C.; Williams, A.F.; Barclay, A.N. J. Biol. Chem. 265, 10410-10418, 1990 A;Title: High level expression in Chinese hamster ovary cells of soluble forms of CD4 T. A;Reference number: A35433; MUID:90285164; PMID:2113054
                                                                                                                                                                                     A;Cross-references: EMBL:X72453; NID:g441374; PIDN:CAA51121.1; PID:g441375 (?Superfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;36-110/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                          Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi
A;Reference number: S40312; MUID:94080891; I
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change
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A; Residues: 1-457 < CLA>
                                                                                                                                                                                                                                                                                 A; Residues:
                                                                                                                                                                                                                                                                                                        A; Molecule type: mRNA
                                                                                                                                                                                                                                                                                                                              A; Status: preliminary; translation
                                                                                                                                                                                                                                                                                                                                                                                                                                                 R; Klein, R.; Jaenichen, R.; Zachau, H.G.
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                                                                                                                Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Species: Homo sapiens (man)
                                                                                               Matches
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EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPTVLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DSGTWTCTVLONOKKVEFKIDIVVLAFOKAS 208
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                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19.1%; bu
49.3%; Pred
49.3%; 34;
                                                                                                                19.0%;
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                                                                                            Score 507; DB 2;
Pred. No. 3.3e-20;
7; Mismatches 3
                                                                                                                                                                                                                                                                                                                                not shown
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PMID:8258341
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447 RFSGSGSGAEFTLTISSLQSEDFAVYYCQQYNNWPPRYTFGQGTRLEIK

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A;Recerence number: S40312; MUID:94080891; PMID:8258341
A;Accession: S40362
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Eur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40362
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C;Species: Homo sapiens (man)
C;Date: 02-Dec_1993 #sequence_revision 10-Nov-1995 #text_change 21-Jan-2000
T-cell surface glycoprotein CD4 precursor - mouse N_rAlternate names: T-cell differentiation antigen C_rSpecies: Mus musculus (house mouse)
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A;Molecule type: mRNA
A;Residues: 1-107 - KMAR>
A;Cross-references: EMBL:Z18330
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A; Title: Nucleotidic sequence analysis of the variable domains A; Reference number: S34001; MUID:93209281; PMID:7681398
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                                                             RWMST'
                                                                             RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                             1-117 <KLE>
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ain: immunoglobulin homology
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Similarity 88.1%;
                                                                                                                                                               RFSGSGSGAEFTLTISSLQSEDFAVYYCQQYNNWPPRYTFGQGTRLEIK 495
                                                                                                                                                                                                            RESGSGSGTEETLTISSLQSEDFAVYYCQQYRNWP--RTFGQGTKVEIK 107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA
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                                                                                                                                                                                                                                                                                                                                                                    immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                            Conservative
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88.1%;
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Pred. No. 8.9e-20;
7; Mismatches 4
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Pred. No. 8.2e-20;
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                       L3T4;
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                       T4/Leu
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A;Molecule type: DNA
A;Residues: 1-25, 'E',27-457 <GOR>
A;Residues: 1-25, 'E',27-457 <GOR>
A;Crose-references: GB:M17080; GB:J03003; NID:g192515; PIDN:AAA37402.1; PID:g387124
A;Crose-references: GB:M17080; GB:J03003; NID:g192515; PIDN:AAA37402.1; PID:g387124
R;Maddon, P.J.; Molineaux, S.M.; Maddon, D.E.; Zimmerman, K.A.; Godfrey, M.; Alt, F.W.;
Proc. Natl. Acad. Sci. U.S.A. 84, 9155-9159, 1987
Proc. Natl. Acad. Sci. U.S.A. 84, 9155-9159, 1987
A;Title: Structure and expression of the human and mouse T4 genes.
A;Reference number: A39955; MUID:88097446; PMID:3501122
A;Accession: A39955
                                     F;139-190/Domain: immunoglobulin homology #status atypical <IM2>
F;220-301/Domain: immunoglobulin homology <IM3>
F;221-457/Product: CD4, brain-specific short form #status predic
F;221-372/Domain: immunoglobulin homology <IM4>
F;321-372/Domain: immunoglobulin homology <IM4>
F;395-419/Domain: transmembrane #status predicted <IM7>
F;420-457/Domain: intracellular #status predicted <INT>
F;42-112,159-188,328-370/Disulfide bonds: #status predicted
                                                                                                                                                                                                                                                                                                                                                                                                                                                              C;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology C;Keywords: alternative initiators; duplication; glycoprotein; T-cell; transf;126/Domain: signal sequence #status predicted sSIG> F;27-457/Product: T-cell surface glycoprotein CD4 #status experimental <MAT> F;35-114/Domain: immunoglobulin homology <MM1>
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A;Cross-references: GB:M36851; NID:g198672; PIDN:AAA39402.1; PID:g554183
A;Cross-references: GB:M36851; NID:g198672; PIDN:AAA39402.1; PID:g554183
A;Classon, B.J.; Tsagaratos, J.; Kirszbaum, L.; Maddox, J.; Mackay, C.R.; Brandon, Mackay, C.R.; Brando
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A;Title: L3T4 and the immunoglobulin gene superfamily: |
A;Reference number: I54564; MUID:88152875; PMID:3326818
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N;Littman, D.R.; Gettner, S.N.
Nature 325, 453-455, 1987
A;Title: Unusual intron in the immunoglobulin domain of the newly isolated mu A;Reference number: A26038; MUID:87115821; PMID:3027575
A;Reference number: A26038; MUID:87115821; PMID:3027575
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A;Residues: 1-457 <RES>
A;Cross-references: GB:M36850; NID:g198670;
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A; Residues: 1-457 < TOU>
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A; Residues: 25-457 < MAD>
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A; Residues: 1-457 <LIT>
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(covalent)
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Ig kappa chain - human

C;Species: Homo sapiens (man)

C;Species: Homo sapiens (man)

C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000

C;Accession: $40378

R;Klein, R.; Jaenichen, R.; Zachau, H.G.

Eur: J. Immunol. 23, 3248-3271, 1993

A;Title: Expressed human immunoglobulin chi genes and their hypermutation.

A;Reference number: $40312; MUID:94080891; PMID:8258341

A;Recession: $40378

A;Recession: $40378

A;Recession: $40312; MUID:94080891; PMID:8258341

A;Residue: preliminary; translation not shown

A;Residues: 1-123 <KLE>

A;Cross-references: EMBL:X72488; NID:9441444; PIDN:CAA51156.1; PID:9441445

C;Superfamily: immunoglobulin V region; immunoglobulin homology

C;Keywords: heterotetramer; immunoglobulin

F;29-103/Domain: immunoglobulin homology <IMM>
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S40378
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(Species: Homo sapiens (man)
(C;Species: Homo sapiens (man)
C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 21-Jan-2000
C;Accession: B26555
R;Middaugh, C.R.; Litman, G.W.
J. Biol. Chem. 262, 3671-3673, 1987
A;Title: Atypical glycosylation of an IgG monoclonal cryoimmunoglobulin.
A;Reference number: A92630; MUID:87137666; PMID:3102493
A;Accession: B26555
A;Molecule type: protein
A;Residues: 1-116 -MID>
C;Superfamily: immunoglobulin V region; immunoglobulin homology
C;Keywords: heterotetramer; immunoglobulin
F;16-90/Domain: immunoglobulin homology <IMM>
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Search completed: September 20, 2005, 16:10:09 Job time : 36 secs

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FROM N.A. =96303695; PubMed=872 Lari M.A., Muzny D.M. F., Gibbs R.A.; rich cluster between thuman chromosome 12 Res. 6:314-326(1996). B FROM N.A., AND VARI =91216786; PubMed=170 W., Sasso D.R., McDo with OKT4-epitope de in the CD4 gene, resu munol. 30:99-104(1991 E FROM N.A. Pancreas; =22388257; PubMed=124 E FROM N.A. Pancreas; 12388257; PubMed=124 E FROM N.A. Pancreas; 12388257; PubMed=124 E FROM N.A. Pancreas; 12388257; PubMed=124 E FROM N.A. Pancreas; 13 F.F., Jordan H., Moo R.F., Jordan H., Moo R.F., Jordan H., Moo R.F., Joares M.B., B. R.F., Jordan H., Moo R.F., Joares M.B., B. E M.T. B. FROM N.B. R.F., Jordan H., Moo R.F., Joares M.B., B. FROM N.B. FROM N.B. R.F., Jordan H., Moo R.F., Jordan H., Moo R.F., Jordan H., Moo R.F., Jordan H., Moo	y4; pta; Metazoa; Cho a; Eutheria; Pri xID=9606; E FROM N.A. D=85254948; PubMe P.J., Littman D. solation and nucl protein T4: a n	STANDARD; 6 (Rel. 01, Crea 8 (Rel. 09, Last 5 (Rel. 46, Last face glycoprotei	22.3 22.1 21.9 21.1 21.1 21.1 119.1 118.9 118.7 118.7 118.7 118.7 118.7 118.7 118.7
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hosphate isomerase hosphate isomerase 98-8859(91)90077-M; 98-8859(91)90077-M; le nucleotide base n of TRP240 for C.F., Bhat N.K., ge J.G., Bat N.K., g.J., Heich F., M., Hong L., T.L., Scheetz T.E., T.L., Scheetz T.E.,	ae; Homo. Chess L., Axel R.; encoding the T cell culin gene family."; 2-8674(88)90211-5;	surface antigen	Q61bkl canis famil P79355 felis silve Q69yr3 sus scrofa Q673n3 sus scrofa Q673n3 sus scrofa Q673n4 sus scrofa P05540 rattus norv P04207 homo sapien P06332 mus musculu Q61396 mus musculu Q61396 homo sapien P01624 homo sapien P01624 homo sapien Q9ul83 homo sapien Q9ul83 homo sapien Q9ul83 homo sapien Q9ul83 homo sapien Q50mw0 homo sapien Q50mw0 homo sapien

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Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,

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BOBBA S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren E.J., Lu X., Gibbs R.A., Fahey J., Helton B., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grimwood J., Schmutz J., Myers R.M., Butterfield Y.S.N., Krzywinski M.I., Skalska U., Smailus D.E., Schnerath A., Schein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length huma and mouse cDNA sequences.";
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"Cloning and sequences of primate CD4 molecules: diversity cellular receptor for simian immunodeficiency virus/human immunodeficiency virus.";
Eur. 7 Terminodeficiency virus.";
                                                                                                                                                                                                                                        X-RAY CRYSTALLOGRAPHY (2.3 ANGSTROMS) OF 26-208.
MEDLINE=91061882; PubMed=2247146; DOI=10.1038/348419a0;
RYU S.-E., Kwong P.D., Trunch A., Porter T.G., Arthos J.,
Rosenberg M., Dai X., Xuong N.-H., Axel R., Sweet R.W.,
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MEDLLNE-91061881; PubMed=1701030; DOI=10.1038/348411a0;
Wang J., Yan Y., Garrett T.P., Liu J., Rodgers D.W., Garlic's
Tarr G.E., Husain Y., Reinherz E.L., Harrison S.C.;
"Atomic structure of a fragment of human CD4 containing two
immunoglobulin-like domains.";
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"Signal peptide mana"
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                                                                                                               MEDLINE=97311402; PubMed=9168119;
Wu H., Kwong P.D., Hendrickson W.
                                                                                                                                                                                                                            Rosenberg M., Dai
Hendrickson W.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REMOVAL FROM CELL SURFACE SER-433; 438-LEU-LEU-439;
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   MEDLINE=92317088;
Crise B., Rose J.I
                                                                                                                                                               Nature 348:419-426(1990).
[12]
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                                 PALMITOYLATION
                                                                 Nature
                                                                                human
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PubMed=8124721;
                                                                                                 "Dimeric
                                                                                                                                                                                                         "Crystal structure of an HIV-binding recombinant fragment
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                                                                                CD4.";
                                                                 387:527-530(1997)
                                                                                                                                                                                                                                                                                                                            348:411-418(1990).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              virus.";
22:2973-2981(1992).
                    PubMed=1618861;
                                                                                                                Hendrickson W.A.;
                                                                                               and
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                                                                                               segmental variability in the structure
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PIR; A90872; RWHUT4.

PDB; 1CDH; X-ray; @=25-203

PDB; 1CDJ; X-ray; @=26-203

PDB; 1CDJ; X-ray; @=26-203

PDB; 1CDJ; X-ray; @=26-203

PDB; 1CDV; X-ray; @=26-203

PDB; 1G9N; X-ray; C=26-210

PDB; 1G9N; X-ray; C=26-210

PDB; 1G9N; X-ray; C=26-210

PDB; 1G9N; X-ray; C=26-210

PDB; 1G9N; X-ray; D=26-203

PDB; 1G9N; X-ray; D=26-203

PDB; 1MBR; NMR; A=421-458.

PDB; 1WBR; NMR; @=427-445.

PDB; 1WBY; X-ray; A/B=26-3

PDB; 1WIQ; X-ray; A/B=26-3

PDB; 1WIQ; X-ray; A/B=26-3

PDB; 3CD4; X-ray; A/B=26-3

PDB; 3CD4; X-ray; 0=26-207

G1yCoSuiteDB; PDT30; -

Genew; HGNC:1678; CD4.
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MIM; 18694
GO; GO:004
GO; GO:001
GO; GO:001
GO; GO:004
DOMAIN
TRANSMEM
DOMAIN
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EMBL; U47924; AAB51309.1; -.
EMBL; M35160; AAA16069.1; -.
EMBL; BC025782; AAH25782.1; -.
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J. Biol. Chem. 267:13593-13597(1992).
                                                              Polymorphism;
SIGNAL
                                                                                               PROSITE; PS50835; IG_LIKE; 1.
3D-structure; Direct protein sequencing; Glycoprotein;
Immune response; Immunoglobulin domain; Lipoprotein; P
                                                                                                                                                   PRINTS; PR00692; CD4;
SMART; SM00406; IGv;
                                                                                                                                                                                               InterPro; IPR008424; CD2.
InterPro; IPR000973; CD4 TCAg.
InterPro; IPR0071110; Ig-like.
InterPro; IPR003556; Ig_v.
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                                                                                                                                                                                                                                                                  GO:0005886; C:plasma membrane; TAS.
GO:0042101; C:T-cell receptor complex; NAS.
GO:0015026; F:coreceptor activity; NAS.
GO:0015026; F:internalization receptor activity; TAS.
GO:0015029; F:internalization receptor activity; TAS.
GO:0042289; F:MTC class II protein binding; NAS.
GO:0004289; F:transmembrane receptor activity; TAS.
GO:0004505; P:immune response; NAS.
GO:0006955; P:immune response; NAS.
GO:0045086; P:positive regulation of interleukin-2 biosyn.
GO:0045086; P:T-cell selection; NAS.
GO:0045058; P:T-cell selection; NAS.
GO:0045058; P:T-cell selection; NAS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3; 1Q68; NMR; A=421-458.

3; 1WBR; NMR; @=427-445.

3; 1WIO; X-ray; A,B=26-388.

3; 1WIP; X-ray; A,B=26-388.

3; 1WIQ; X-ray; A,B=26-388.

3; 1WIQ; X-ray; @=26-207.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Type I membrane protein. Removed from plasma membrane by HIV-1 Nef protein that increases clathrin-dependent endocytosis of this antigen to target it to lysosomal degradation. SIMILARITY: Contains 3 immunoglobulin-like C2-type domains. SIMILARITY: Contains 1 immunoglobulin-like V-type domain. SIMILARITY: Contains 1 immunoglobulin-like V-type domain. DATABASE: NAME=PROW; NOTE=CD guide CD4 entry; WWW#="http://www.ncbi.nlm.nih.gov/prow/cd/cd4.htm".
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X-ray, C=26-210.

X-ray, C=26-210.

X-ray, C=26-203.
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X-ray; @=26-203.
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X-ray; @=25-203.
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26
397
419
                                                                                 Repeat;
                                                                                                                                                                      CD4TCANTIGEN.
Signal;
Potential.
Cytoplasmic
                                               T-cell surface
                                 Extracellular
                                                                                   T-cell;
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Best Local Sim
Matches 208;
                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-93049640; PubMed-1425921;

Fomsgaard A., Hirsch V.M., Johnson P.R.;

Fomsgaard A., Hirsch V.M., Johnson P.R.;

Collular receptor for simian immunodeficiency virus/human immunodeficiency virus/human immunodeficiency virus and immunodeficiency virus.

Eur. J. Immunol. 22:2973-2981(1992).

-I- FUNCTION: Accessory protein for MHC class-II antigen/T-cell activation.
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01-APR-1990 (Rel
05-JUL-2004 (Rel
T-cell surface g
T4/Leu-3)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       "A CD4 domain important for HIV-mediated syncytium formation lies outside the virus binding site.";
Cell 60:747-754(1990).
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P16004;
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MEDLINE=90182664; PubMed=2107024;
Camerini D., Seed B.;
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Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
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DOMAIN
                    EMBL; M31135; AAA35407.1;
EMBL; X73323; CAA51749.1;
PIR; B32722; RWCZT4.
                                                                                                                                                            use by non-profit institutions as long modified and this statement is not removed.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Name=CD4;
                                                                                                                                                                                                                                                                                                           receptor interaction. May regulate T-cell activation. SUBUNIT: Associates with p56-lcb (By similarity). SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: Contains 3 immunoglobulin-like C2-type domains. SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                       s SWISS-PROT entry is copyright. It is produced through a collaboration ween the Swiss Institute of Bioinformatics and the EMBL outstation - Buropean Bioinformatics Institute. There are no restrictions on its by non-profit institutions as long as its content is in no way
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                                                                                                                 s requires a license agreement ( an email to license@isb-sib.ch)
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126
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44,
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Pred. No. 1.8e-59;
0; Mismatches 0;
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Ig-like
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                                                                                                                                                                                                                                                                       MACFA
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PRINTS; PR00692; CD4TCANTIGEN
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                                                                          Name=CD4;
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PROSITE; PS50835; IG_LIKE; 1.
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InterPro; IPR000973;
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InterPro; IPR003596;
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GO:0015026; F:coreceptor activity; ISS.
GO:0042289; F:MfC class II protein binding; ISS.
GO:0006955; P:immune response; ISS.
GO:0045086; P:positive regulation of interleukin-2
GO:0045086; P:T-cell differentiation; ISS.
GO:0045086; P:T-cell selection; ISS.
GO:0045086; P:T-cell selection; ISS.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ILGNQGSFLTKGPSKLNDRADSRRSLMDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                                                                                                   (Rel. 36, Created)
(Rel. 36, Last sequence update)
(Rel. 44, Last annotation update)
ace glycoprotein CD4 precursor (T-
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By similarity.
S-palmitoyl cysteine (
S-palmitoyl cysteine (
S-palmitoyl cysteine (
T-> N (in Ref. 2).
L-> S (in Ref. 2).
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Ig-like V-type.

Ig-like C2-type 1.

Ig-like C2-type 2.

Ig-like C2-type 3.

Ig-like C2-type 3.

N-linked (GlCNAc...
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Pred. No. 5
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Extracellular (Potential).
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T-cell surface
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Macaca fascicularis Eukaryota; Metazoa; Mammalia; Eutheria;

(Crab eating macaque) Chordata; Craniata; V Primates; Catarrhini;

e) (Cynomolgus monkey).Vertebrata; Euteleostomi;i; Cercopithecidae;

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Query Match
Best Local S
Matches 185
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EMBL; D63349; BAA09673.1; -..
HSSP; P01730; IMBR.
GO; GO:0042101; C:T-cell receptor
GO; GO:0015026; F:coreceptor act
GO; GO:0015026; F:coreceptor act
GO; GO:0042289; F:MHC class II p.
GO; GO:0045086; P:positive regula
GO; GO:0045086; P:positive regula
GO; GO:0030217; P:T-cell differen
GO; GO:0045086; P:T-cell selective
GO; GO:0045086; P:T-cell selective
GO; GO:0045086; P:T-cell selective
GO; GO:0007169; P:transmembrane
InterPro; IPR00973; CD2.
InterPro; IPR00973; CD4 TCAg.
InterPro; IPR00973; GJ Tike.
InterPro; IPR00973; GJ Tike.
InterPro; IPR0003596; Ig_v.
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Pfam; PF00047; ig; 2.
DB00692; CD4TCANTIGEN.
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PROSITE; PS50835; IG_LIKE; 1.
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Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GO:0042101; C:T-cell receptor complex; ISS.
GO:0015026; F:coreceptor activity; ISS.
GO:00150289; F:MfC class II protein binding; ISS.
GO:0006955; P:immune response; ISS.
GO:0006955; P:positive regulation of interleukin-2 biosyn.
GO:0045086; P:positive regulation; ISS.
GO:0030217; P:T-cell differentiation; ISS.
GO:0045088; P:T-cell selection; ISS.
GO:0045088; P:Transmembrane receptor protein tyrosine kin.
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                                                                    61
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SM00406; IGV;
                                                                                                                                                                                                                                                                                                                            Similarity
                                      MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
ILGIQGSFLTKGPSKLSDRADSRKSLWDQGCFSMIIKNLKIEDSDTYICEVENKKEEVEL
                                                                                                                                         MNRGIPFRHLLLVLQLALLPAVTQGKKVVLGKKGDTVELTCNASQKKNTQFHWKNSNQIK
                                                                                                                                                                                                                                                                                          Conservative
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By similarity.
T-cell surface glycoprotein CD4.
Extracellular (Potential).
Potential.
Cytoplasmic (Potential).
Ig-like V-type.
Ig-like C2-type 1.
Ig-like C2-type 3.
Ig-like C2-type 3.
Ig-like C2-type 3.
N-linked (GlcNAc. . ) (By similar N-linked (GlcNAc.
                                                                                                                                                                                                                                                                                      12;
                                                                                                                                                                                                                                                                                  Score 953; DE
Pred. No. 1.9e
L2; Mismatches
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.9e-52;
                                                                                                                                                                                                                                                                                                                                                          Length
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(By similarity)
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similarity).
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CD4_MACFU
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TRANSMEM
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PRINTS; PR00692; CD4TCANTIGEN.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                  InterPro; IPR008424; CD2.
InterPro; IPR000973; CD4 TCAg.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR003596; Ig_v.
                                                                                                                                                                                                                                                                                                                                                                                 the European Bioinformatics Institute. The use by non-profit institutions as long a modified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Event the European Bioinformatics Institute. There are no restructed by non-profit institutions as long as its content
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Cercopithecinae; Macaca.
NCBI_TaxID=9543;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Macaca fuscata fuscata (Japanese macaque)
Eukaryota; Metazoa; Chordata; Craniata; V
Mammalia; Eutheria; Primates; Catarrhini;
                                                                                                                  Glycoprotein;
Palmitate; Re
                                                                                                                                                                                                                                                                                                                                                            entities requires a license agreement (S or send an email to license@isb-sib.ch).
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Hashimoto O., Tatsumi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T4/Leu-3).
                                                                                                                                                                                                                                 GO:0042101; C:T-cell receptor complex; ISS.
GO:0012026; F:coreceptor activity; ISS.
GO:0042209; F:MC class II protein binding; ISS.
GO:0006955; P:immune response; ISS.
GO:0045086; P:positive regulation of interleukin-2 biosyn.
GO:0030217; P:T-cell differentiation; ISS.
GO:0045086; P:T-cell selection; ISS.
GO:0045086; P:T-cell selection; ISS.
GO:0045086; P:T-cell selection; ISS.
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P01730;
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(Rel. 36, Last sequence update)
(Rel. 44, Last annotation update)
ace glycoprotein CD4 precursor (T-cell
                                                                                                               Immune responeat; Signal;
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1WBR.
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                                                                                                                  response; Immi
Potential.

Cytoplasmic (Potential).

Ig-like V-type.

Ig-like C2-type 1.

Ig-like C2-type 2.

Ig-like C2-type 3.

N-linked (GlCNAc...) ()
                                                                                By similarity.
T-cell surface of
Extracellular ()
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                                                                                                                             Immunoglobulin domain; Lipoprotein;
                                                                                                                  Transmembrane.
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                                                                                 e glycoprotein (Potential).
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Best Local S
Matches 184
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P16003; Q29617;
01-APR-1990 (Rel. 14, Created)
28-FEB-2003 (Rel. 41, Last sec
05-JUL-2004 (Rel. 44, Last and
T-cell surface glycoprotein C
                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.
TISSUE=Thymnocytes;
Hashimoto O., Tatsumi M.;
"Molecular cloning and expi
Submitted (JUN-1995) to the
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                                                                                                                                                   Foomsgaard A., Hirsch V.M., Johnson P.R.; "Cloning and sequences of primate CD4 molecules: diversity of the cellular receptor for simian immunodeficiency virus/human immunodeficiency virus.";
                                                                                                                                                                                                                                                                                                                                                                                                                                           outside the virus bind Cell 60:747-754(1990). [2]
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Cercopithecinae; Macaca.
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Eukaryota; Metazoa; Chordata; Cr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Name=CD4;
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                  Harris E.E., Disotell T.R., "Nuclear gene trees and the phylogenetic
                                                                                                                                                                                                                                                                TISSUE=Blood
                                                                                                                                                                                                                                                                                   SEQUENCE OF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Primates; Catarrhini;
                                                               MEDLINE=98320644;
                                                                                        SEQUENCE
                                                                                                                                                                                                                                       MEDLINE=93049640; PubMed=1425921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CD4 domain important for HIV-mediated syncytium tside the virus binding site.";
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PubMed=2107024; DOI=10.1016/0092-8674(90)90089-W; B.;
                                                               PubMed=9656488;
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  Papionini).";
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o the EMBL/GenBank/DDBJ databases.
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N-linked (GlcNAC. ..) (By
By similarity.
By similarity.
By similarity.
S-palmitoyl cysteine (By s
S-palmitoyl cysteine (By s
S-palmitoyl cysteine (By s
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Pred. No. 2.6e-52;
3; Mismatches 11;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Craniata; Vertebrata; Euteleostomi;
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Best Local S
Matches 183
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R GO; GO:0042101; C:T-cell receptor complex; ISS.

R GO; GO:0015026; F:coreceptor activity; ISS.

R GO; GO:0015026; F:coreceptor activity; ISS.

R GO; GO:0042289; F:MHC class II protein binding; ISS.

R GO; GO:0006955; P:immune response; ISS.

R GO; GO:0045086; P:positive regulation of interleukin-2 bio GO:0045017; P:T-cell differentiation; ISS.

R GO; GO:0030217; P:T-cell differentiation; ISS.

R GO; GO:0045058; P:T-cell selection; ISS.

R GO; GO:0007169; P:transmembrane receptor protein tyrosine R InterPro; IPR000424; CD2.

R InterPro; IPR000424; CD2.

R InterPro; IPR000424; CD2.
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                                                                                             SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                   Glycoprotein; Immune
Palmitate; Repeat; S:
                                                                                                                                                                                                                                                                                                                                                                                                                          SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                Pfam; PF00047; ig; 2.
PRINTS; PR00692; CD4TCANTIGEN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       -i- FUNCTION: Accessory protein for MHC class-II antigen/T-ce receptor interaction. May regulate T-cell activation.
-i- SUBUNIT: Associates with p56-lck (By similarity).
-i- SUBCELLULAR LOCATION: Type I membrane protein.
-i- SIMILARITY: Contains 3 immunoglobulin-like C2-type domain.
-i- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            M31134; AAA36838.1;
D63347; BAA09671.1;
X73326; CAA51752.1;
                         -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            s requires a license agreement (S an email to license@isb-sib.ch).
                                                            Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; IPR008424; CD2.
; IPR000973; CD4_TCAg.
; IPR007110; Ig-Tike.
; IPR003596; Ig_v.
             MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKS1QFHWKNSNQIK
MNRGI PFRHLLLVLQLALLPAVTQGKKVVLGKKGDTVELTCNASQKKNTQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                   Repeat; Signal;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Evol. 15:892-900(1998)
                                                                                                          266
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                                                                                                                     50884
                                                          35.4%;
                                                                                                                                                                                                                                                                                                                                                                                                               response; Immunoglobulin domain; Lipoprotein;
                                                                                                MW.
                                                                                                                                                                                                                                                                                                                                                                                                   T-cell; Transmembrane
                                                                                                      By similarity.
By similarity.
By similarity.
By similarity.
Systeine (
S-palmitoyl cysteine (
S-palmitoyl cysteine (
N-> T (in Ref. 1).
L-> S (in Ref. 2).
L-> S (in Ref. 2).
L-> N (in Ref. 2).
S-> P (in Ref. 2).
R-> Q (in Ref. 3).
R-> Q (in Ref. 3).
R-> Q (in Ref. 3).
                                                                                                                                                                                                                                                               Ig-like V-type 1
Ig-like C2-type 1
Ig-like C2-type 2
Ig-like C2-type 2
Ig-like C2-type 3
N-linked (GlCNAC
N-linked (GlCNAC
                                              Score 945; DB
Pred. No. 6.2e
.3; Mismatches
                                                                                                                                                                                                                                                                                                                                        Potential.
Cytoplasmic
                                                                                                                                                                                                                                                                                                                                                               T-cell surface glycoprotein Extracellular (Potential).
                                                                                                8BB80339FAFEC808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for MHC class-II antigen/T-cell
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (See http://www.isb-sib.ch/announce/
                                                          DB 1;
.2e-52;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       protein tyrosine
                                                                                                                                                                                                                                                                                                                                         (Potential).
                                                12;
                                                                                               CRC64;
                                                                      Length
                                                Indels
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УВ)
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(By
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similarity)
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similarity).
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Q08340; P79196;
01-FEB-1995 (Rel. 31, Created
15-JUL-1998 (Rel. 36, Last se:
05-JUL-2004 (Rel. 44, Last an:
T-cell surface glycoprotein C
T4/Leu-3).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MACNE
                                                                                                                                                                             EMBL;
EMBL;
HSSP;
GO; GO
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GO; GO
GO; GO
GO; GO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Fomsgaard A., Hirsch V.M., Johnson P.R.; Cloning and sequences of primate CD4 molecules: diversity cellular receptor for simian immunodeficiency virus/human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE FROM N.A. Hashimoto O., Tatsumi Submitted (FEB-1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Cercopithecinae; Macaca.
NCBI_TaxID=9545;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              immunodeficiency virus.";
Eur. J. Immunol. 22:2973-2981(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDLINE=93049640; PubMed=1425921;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE OF 28-424 FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Macaca nemestrina (Pig-tailed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Name=CD4;
                                                                                                                                                                        GO:0042101; C:T-cell receptor complex; ISS.
GO:0015026; P:coreceptor activity; ISS.
GO:00142289; F:MfC class II protein binding; ISS.
GO:0042289; F:MfC class II protein binding; ISS.
GO:0006955; P:immune response; ISS.
GO:0045086; P:positive regulation of interleukin-2
GO:0045086; P:T-cell differentiation; ISS.
GO:0045088; P:T-cell selection; ISS.
GO:0007159; P:transmembrane receptor protein tyrosi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation. SUBUNIT: Associates with p56-lck (By similarity). SUBCELLULAR LOCATION: Type I membrane protein. SIMILARITY: Contains 3 immunoglobulin-like C2-type domains. SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         181
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                                                                                                                                                                                                                                                                                                                                                                                 D63346; BAA09670.1; -. X73325; CAA51751.1; -. P01730; 1WBR.
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                                                           ); IPR008424; CD2.
); IPR000973; CD4 TCAg.
); IPR007110; Ig-Tike.
); IPR003596; Ig_v.
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2; CD4TCANTIGEN
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annotation update)
n CD4 precursor (T-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  l macaque).
; Craniata; Vertebrata; Euteleostomi;
· Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRT;
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Best Local :
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Glycoprotein; Immu
Palmitate; Repeat
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TWTCTVSQDQKTVBFKIDIVVLAFQKAS
                     TWTCTVLQNQKKVEFKIDIVVLAFQKAS 208
                                                                                      LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKN1QGGKTLSVSQLELQDSG
                                                                                                                                                      ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFFLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                            MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                          MNRGIPFRHLLLVLQLALLPAVTQGKKVVLGKKGDTVELTCNASQKKNTQFHWKNSDQIK
                                                                     LVFGLTANSDTHLLEGQSLTLTLESPPGSSPSVKCRSPGGKNIQGGRTLSVPQLERQDSG
                                                                                                                                        ILGIQGSFLTKGPSKLSDRADSRKSLWDQGCFSMIIKNLKIEDSNTYICEVENEKEEVEL
                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                                                                                                                                                                                                                                         14;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T-cell; Transmembrane.
                                                                                                                                                                                                                                                                                                                                                          Cytoplasmic (Potential Ig-like V-type 1. Ig-like C2-type 1. Ig-like C2-type 2. Ig-like C2-type 3. N-linked (GlcNAc. .) N-linked (GlcNAc. .) N-linked (GlcNAc. .) N-linked (GlcNAc. .) By similarity. By similarity. By similarity cysteine (S-palmitoyl cysteine (S-palm
                                                                                                                                                                                                                                                                                             Score
Pred.
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No. 7
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                                                                                                                                                                                                                                                                                           DB 1;
.2e-52;
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similarity)
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RESULT
CD4_CER
RRRRR ROCCOGNETT
                                                                                                                                                                                                                                                                                      _CERAE
                                                                                                                                                                               CD4_CERAE STANDARD; PKT; 455 An. (208338; O02805; O77593; Q28217; O1-FEB-1995 (Rel. 31, Created) 29-MAR-2004 (Rel. 43, Last sequence update) 05-JUL-2004 (Rel. 44, Last annotation update) 1-cell surface glycoprotein CD4 precursor (T-cell T4/Leu_3).
                                     Hashimoto O., Tatsumi N
"Molecular cloning and
Submitted (JUL-1996) to
                                                                                                                                     Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Eutel
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae
SEQUENCE OF 3
                                                                               SEQUENCE FROM N.A.
                                                                                                        Cercopithecinae; Cercopithecus.
NCBI_TaxID=9534;
             28-424
             FROM N.A
                                        ö
                                                                  Σ
:
                                       expression the EMBL/
                                        assion of african green monkey CD4."; EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                           surface antigen
                                                                                                                                                     Euteleostomi;
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MEDLINE=93049640; PubMed=1425921;

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SIGNAL
CHAIN
DOMAIN
TRANSMEM
DOMAIN
DOMAIN
DOMAIN
DOMAIN
CARBOHYD
DISULFID
                                                                                                                                                                                                                                                                                                              InterPro; 15...
Pfam; PF00047; 19; 2.
PRINTS; PR00692; CD4TCANTIGEN.
PROSITE; PS50835; IG LIKE; 1.
PROSITE; PS50835; IG LIKE; IG 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HSSP; P01730; IWIQ.

G0; G0:0042101; C:T-cell receptor complex; ISS.

G0; G0:0015026; F:correceptor activity; ISS.

G0; G0:0012289; F:MHC class II protein binding; ISS.

G0; G0:0042289; F:immune response; ISS.

G0; G0:0045086; P:positive regulation of interleukin-2

G0; G0:0030217; P:T-cell differentiation; ISS.

G0; G0:0030217; P:T-cell differentiation; ISS.

G0; G0:0045088; P:T-cell selection; ISS.

G0; G0:0045088; P:transmembrane receptor protein tyrosi
Interpro; IPR008424; CD2.
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EMBL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -:- FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation.
-:- SUBUNIT: Associates with p56-lck (By similarity).
-:- SUBCELLULAR LOCATION: Type I membrane protein.
-:- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
-:- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "Nuclear gene trees and the phylogenetic relationships of mangabeys (Primates: Papionini).";
Mol. Biol. Evol. 15:892-900(1998).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fomsgaard A., Mueller-Trutwin M.C., Diop O., Hansen J., Corbet S., Barre-Sinoussi F., Allan J.S.; Relation between phylogeny of African green monkey CD4 their respective simian immunodeficiency virus genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Fomsgaard A., Hirsch V.M., Johnson P.R.; "Cloning and sequences of primate CD4 molecules: diversit cellular receptor for simian immunodeficiency virus/human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Harris E.E., Disotell T.R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MEDLINE=98320644;
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MEDLINE=98017879; PubMed=9379478;
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IPR000973; CD4_TCAg.
IPR007110; Ig-Tike.
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20644; PubMed=9656488;
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       By similarity.

T-cell surface glycoprotein Cl
Extracellular (Potential).
Potential.
(Cytoplasmic (Potential).
Ig-like V-type.
Ig-like C2-type 1.
Ig-like C2-type 3.
Ig-like C2-type 3.
Ig-like C2-type 3.
N-linked (GlCNAc. . .) (Potential)
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orimate CD4 molecules: diversity
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SMART; SM00409; IG; 2.
SMART; SM00406; IGv; 2
PROSITE; PS50835; IG_L
                                                                                                                                                                                                                                              InterPro; IPR003599; Ig.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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EMBL; Y13057; CAA73500.1; -.
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                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
MEDLINE=97362799; PubMed=9219263;
                                                                                                                                                                                                                                                                                                                                                                                                                                          Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Homo sapiens (Human)
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QVQLVQSGAEVKKPGDSVKVSCKASGYTFSDHYMHWVRQAPGQGLEWMGWIDPNNGDTRF
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244 AA;
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i; Hominidae; Homo.
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Fomsgaard A., Hirsch V.M., Johnson P.R.;
"Cloning and sequences of primate CD4 molecules: diversity of
cellular receptor for simian immunodeficiency virus/human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Eukaryota; Metazoa;
Mammalia; Eutheria;
Cercopithecinae; Ce
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Name=CD4;
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EMBL; X73327; CAA51753.1; -.
EMBL; Z73327; CAA51753.1; -.
EMBL; Z73327; CAA51753.1; -.
GO; GO:0042101; C:T-cell receptor complex; ISS.
GO; GO:0042289; F:MHC class II protein binding; ISS.
GO; GO:0042289; F:MHC class II protein binding; ISS.
GO; GO:0045086; P:immune response; ISS.
GO; GO:0045086; P:positive regulation of interleukin-2 binding; GO:0045086; P:T-cell differentiation; ISS.
GO; GO:0045058; P:T-cell differentiation; ISS.
GO; GO:0045058; P:T-cell selection; ISS.
GO; GO:0045058; P:T-cell selection; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunodeficiency virus.";
Eur. J. Immunol. 22:2973-2981(1992)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NCBI_TaxID=9531;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Cercocebus
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: Contains 3 immunoglobulin-like C2-type domain
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation. SUBUNIT: Associates with p56-lck (By similarity).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            114
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                  p; IPR008424; CD2.
p; IPR008973; CD4 TCAg.
p; IPR007110; Ig-like.
p; IPR003596; Ig_v.
pr003596; Ig_v.
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(Rel. 34, Last sequence update)
(Rel. 44, Last annotation update)
ace glycoprotein CD4 (T-cell surface
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Chordata; Craniata; Vertebrata; Euteleostomi;
Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (See http://www.isb-sib.ch/announce/
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Best Local S
Matches 159
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Q08339;
01-FEB-1995 (Re:
01-FEB-1995 (Re:
05-JUL-2004 (Re:
7-cell surface of
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DOMAIN
MEDLINE=93049640; PubMed=1425921; Fomsgaard A., Hirsch V.M., Johnson P.R.; "Cloning and sequences of primate CD4 molecules: cellular receptor for simian immunodeficiency vir
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CIGIO
                                                                                                                    SEQUENCE FROM
                                                                                                                                                          Cercopithecinae;
NCBI_TaxID=9538;
                                                                                                                                                                                                           Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                      Erythrocebus
                                                                                                                                                                                                                                                                              (Fragment).
Name=CD4;
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Palmitate; Re
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SMART; SM00406;
                                                                                              TISSUE-Blood
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(Rel. 31, Last sequence update)
(Rel. 44, Last annotation update)
ace glycoprotein CD4 (T-cell surface
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                                                                                                                                                                                      Erythrocebus.
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une response; Immunoglobulin domain; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        T-cell;
                                                                                                                                                                                                         (Red guenon) (Cercopithecus patas).
; Chordata; Craniata; Vertebrata; Eutele
; Primates; Catarrhini; Cercopithecidae;
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Ig-like V-type.

Ig-like C2-type 1.

Ig-like C2-type 3.

Ig-like C2-type 3.

N-linked (GLNAC. ..) (Potential).

N-linked (GLNAC. ..) (Potential).

N-linked (GLNAC. ..) (Potential).

N-linked (GLNAC. ..) (Potential).

By similarity.

By similarity.

By similarity.

By similarity.

S-palmitoyl cysteine (By:
S-palmitoyl cysteine (By:
S-palmitoyl cysteine (By:
N-palmitoyl cysteine (B
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Pred. No. 4.5e-44;
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         es: diversity virus/human
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                                                                                                                                                                                                                                   Euteleostomi;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (Potential)
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similarity).
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Query Match
Best Local S
Matches 158
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InterPro; IPR000973; CD4 TCAg.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR003596; Ig_v.
Pfam; PF00047; ig; 2.
PRINTS; PR00692; CD4TCANTIGEN.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PROSITE; PS50835; IG_LIKE; 1.
Glycoprotein; Immune response; Immunoglobulin domain; Lipoprotein;
Palmitate; Repeat; T-cell; Transmembrane.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GO:0042101; C:T-cell receptor complex; ISS.
GO:0015026; F:coreceptor activity; ISS.
GO:0042289; F:MHC class II protein binding; ISS.
GO:00042595; P:immune response; ISS.
GO:0006955; P:positive regulation of interleukin-2 biosyn.
GO:0030217; P:T-cell differentiation; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                . J. Immunol. 22:2973-2981(1992).

FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation. SUBUNIT: Associates with p56-lck (By similarity).

SUBCELLULAR LOCATION: Type I membrane protein.

SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.

SIMILARITY: Contains 1 immunoglobulin-like V-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GO:0045058; P:T-cell selection; ISS. GO:0007169; P:transmembrane receptor
                                                                    148
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                                                                                               DQGCFSMIIKNLKIEDSETYICEVEDKKEEVELLVFGLTANSDTHLLQGQSLTLTLESPP
                                                                                                               DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPP
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Ig-like C2-type 1.
Ig-like C2-type 2.
Ig-like C2-type 3.
Ig-like C4-type 3.
N-linked (GlcNAc. . .) (
N-linked (GlcNAc. . .) (
By similarity.
By similarity.
By similarity.
By similarity.
S-palmitoyl cysteine (By S-palmitoyl cysteine (By
                                                                                                                                                                                                             Score 819; DB 1;
Pred. No. 5.2e-44;
0; Mismatches 13
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Cytoplasmic (Potential).
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Best Local |
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InterPro; IPR007110; Ig-Tike.
InterPro; IPR003196; Ig v.
Pfam; PP05790; C2-8et; 2.
Pfam; PP00047; ig; 1.
PRINTS; PR00692; CD4TCANTIGEN.
SMART; SM00406; IGv; 1.
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01-JUL-1997 (TrE
01-OCT-2003 (TrE
CD4 (Fragment)
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01-JUL-1997
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Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., M

Corbet S., Barre-Sinoussi F., Allan J.S.;

"Relation between phylogeny of African green monkey CD4

"Relation between phylogeny of African green monkey CD4
                                                                                                                                                                                                                                                                                                                                                                                                                                            PROSITE; PS50835; IG_LIKE; 1.
NON TER 1 1
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SEQÜENCE 397 AA; 43945 MW;
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HSSP;
 Name=CD4;
                                                                    009262;
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                            (TrEMBLrel.
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Pred. No. 5.3e-43;
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SEQUENCE 397
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InterPro; IPR000973; CD4 TCAg.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR003596; Igv.
Pfam; PF05790; C2-set; Z.
Pfam; PF006047; ig; I
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O09263;

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O1-JUL-1997 (TrEN:

O1-OCT-2003 (TrEN:

CD4 (Fragment).
SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=88017879; PubMed=9379478;
MEDLINE=88017879; PubMed=9379478;
Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J.
Corbet S., Barre-Sinoussi F., Allan J.S.;
"Relation between phylogeny of African green monkey"
"Relation between phylogeny of African green monkey"
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NCBI_TaxID=60712;
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Mammalia; Eutheria; Primates;
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Mammalia; Eutheria; Primates;
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GO:0007155; P:cell adhesion; II
GO:0006955; P:immune response;
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01-DEC-2001 (TrE
01-DEC-2001 (TrE
01-OCT-2003 (TrE
CD4 (Fragment).
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EMBL;
HSSP;
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HSSP; P01730; 1WIQ.
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P01730; 1
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InterPro; IPRO08424; CD2.
InterPro; IPRO0873; CD4 TCAG.
InterPro; IPRO07110; Ig-Tike.
InterPro; IPRO07110; Ig-Yike.
InterPro; IPRO0710; Ig-Yike.
InterPro; IPRO0716; Ig-Yike.
Pfam; PRO5790; C2-set; Z.
Pfam; PRO0607; Ig-Yike.
PROMET; SMO0406; IG-Yike; 1.
PROSTE; PS50835; IG-YIKE; 1.
InterPro; IPR008424; CD2.
InterPro; IPR000973; CD4 TCAg.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR003596; Igv.
Pfam; PF05790; C2-set; 2.
Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                                             SEQUENCE FROM N.A.

MEDLINE=98017879; PubMed=9379478;
Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J
Corbet S., Barre-Sinoussi F., Allan J.S.;
"Relation between phylogeny of African green monkey
their respective sinian immunodeficiency virus genes
J. Med. Primatol. 26:120-128(1997).
                                                                                                                                                                                                                                                                                                                                                                                                                                                Cercopithecus pygerythrus (Vervet monkey).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata;
Mammalia, Eutheria; Primates; Catarrhini; Cercopithe
Cercopithecinae; Cercopithecus.
                                                                                                                                GO; GO:0016021; C:integral to memb
GO; GO:0007155; P:cell adhesion; I
GO; GO:0006955; P:immune response;
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GO:0007155; P:cell adhesion; IEA.
GO:0006355; P:immune response; IEA.
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(TrEMBLrel.
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Last annotation updat
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Pred. No. !
                                                                                                                                                                              membrane;
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Best Local Similarity
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SEQUENCE
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PRINTS;
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HSSP; P01730; IWIQ.
GO; GO:0016021; C:integral to membrane;
GO; GO:0007155; P:cell adhesion; IEA.
GO; GO:0006955; P:immune response; IEA.
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O09259;
O1-JUL-1997 (TrEMBLrel. 04, Created)
O1-JUL-1997 (TrEMBLrel. 04, Last sequence update)
O1-OCT-2003 (TrEMBLrel. 25, Last annotation update)
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NON_TER 1 1
NON_TER 397 397
SEQÜENCE 397 AA; 43946 MW;
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[1]
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                                                                                                                                                                                                                                PRINTS; PR00692; CD4TCANTIGEN SMART; SM00406; IGv; 1. PROSITE; PS50835; IG_LIKE; 1.
                                                                                                                                                                                                                                                                                                                Pfam; PF05790; C2-set; Pfam; PF00047; ig; 1.
                                                                                                                                                                                                                                                                                                                                            InterPro; IPR008424; CD2.
InterPro; IPR000973; CD4 TCAg.
InterPro; IPR007110; Ig-Iike.
InterPro; IPR003596; Ig v.
Pfam; PF05790; C2-set; Z.
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                                                    155;
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28 VVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLW 87
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                                                                                                                                                     397
397 AA;
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397 AA; 43946 MW; 21C3E30882ABFBC0 CRC64;
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                                                    Conservative
                                                                                                                                                                                                                                                                                             CD4TCANTIGEN
                                                                                                                                                                                      397
                                                                                                                                                           43881 MW;
                                            29.9%; Score 799; DB 2;
85.6%; Pred. No. 9.6e-43;
tive 11; Mismatches 15
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86.2%; Pred. No. 5.3e-43;
tive 10; Mismatches 15; Indels
                                                                                                                                                           7CE39AD0F8506C81 CRC64;
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                                                 15; Indels
                                                                                                   Length 397;
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                                                        GSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLAFQKA
                                                                                                      DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPP
                     S 208
                                             GSSPSVKCRSPRGKNIQGGRTLSVPQLERQDSGTWTCNVSQDQNTVEFKIDIVVLAFQKA
                                                                                         DOGCESMIIKNLKIEDSETYICEVENKEEEVELLVEGLTANSDTHLLOGOSLTLTLESPP
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Search completed: September 20, Job time: 141 secs 2005, 16:09:30 THIS PAGE BLANK (USPTO)

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Title:
Perfect score:
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Listing first 45 summaries
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1 atgaaccggggagtcccttt.....gtcagcagtacaataactgg 1440
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10806.181 Million cell updates/sec
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Copyright (c) 1993 - 2005 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	Score	Query Match	Query Match Length	B	ID	Description
1	1440	100.0	1440	σ,	BD268881	BD268881
N	625	43.4	1213	σ	AR363716	AR363716
ω	624.4	43.4	1377	σ	AX100880	AX100880
4	624.4	43.4	1742	σ	AR380468	AR380468
_U	624.4	43.4	1742	σ	AX287109	AX287109
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7	624.4	43.4	1742	9	HUMATCT4A	M35160
80	624.4	43.4	1910	თ	108116	I08116
9	624.4	43.4	3133	0	I08115	I08115 Sequence
c 10	624.4	43.4	7533	12	AY438650	AY438650 Cloning
11	622.8	43.2	1273	6	I06223	I06223 Sequence
12	622.8	43.2	1273	σ	I07147	I07147 Sequence
13	622.8	43.2	1304	σ	AR067943	AR067943 Sequence
14	622.8	43.2	1304	თ	AR166802	AR166802
15	622.8	43.2	1304	ტ	AR560088	AR560088
16	622.8	43.2	1389	σ	AR062468	AR062468
17	622.8	43.2	1389	σ	AR067924	AR067924
18	622.8	43.2	1389	ტ	AR166783	AR166783
19	622.8	43.2	1389	ש	AR560069	AR560069

ALIGNMENTS

RESULT 1

	OKIGIN
<pre>/organism="synthetic construct" /mol_type="genomic DNA" /db_xref="taxon:32630"</pre>	
11440	source
Location/Qualifiers	FEATURES
FT /organism='Artificial Sequence'.	
source 1	
Location/Qualitiers	
CC Description of Artificial Sequence: CD4-scFv(17b) FH Key	
C12N15/00, C12N5/00, A61K37/02	
PC C07K14/73,C07K16/10,C07K19/00,C12N5/10,C12P21/02//(C12P21/02,	
EDWARD A BERGER, CH	
16-MAR-1999	
	•
PN JP 2002538814-A/1	
OS Artificial Sequence	COMMENT
HEALTH	
DEPARTMENT OF HEALTH AND HUMAN SERVICES THE NATIONAL INSTITUTES OF	
THE AUSTRIAN NORDIC BIOTHERAPEUTICS AKTIENGESELLSCHAFT SECRETARY	
THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY	
Patent: JP 2002538814-A 1 19-NOV-2002;	JOURNAL
infection	
Novel chimeric protein for prevention and treatment of HIV	TITLE
Berger, E.A. and Castillo, C.D.	AUTHORS
1 (bases 1 to 1440)	REFERENCE
other sequences; artificial sequences.	
synthetic construct	ORGANISM
synthetic construct	SOURCE
JP 2002538814-A/1.	KEYWORDS
BD268881.1 GI:33078649	VERSION
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imeric protein for prevention and treatment	DEFINITION
BD268881 1440 bp DNA linear PAT 17-JUL-2003	Locus
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                                          CGACAGGCCCCTGGACAAGGCCTTGAGTGGATGGGAAGGATCATCACTATCCTTGATGTA
                                                                                   CGACAGGCCCCTGGACAAGGCCTTGAGTGGATGGGAAGGATCATCACTATCCTTGATGTA
                                                                                                      GGAGGTTCACAGGTGCAGCTGCTCGAGTCTGGGGCTGAGGTGAAGAAGCCTGGGTCCTCG
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GGAGTGTACGAGGGAGAGGCGGACGAGGGGGGAATATGATAATAATGGGTTTCTGAAACAT
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GCCACCGGTGTCCCAGCCAGGTTCAGTGGCAGTGGGTCTGGGGCAGAATTCACTCTCACC
                                                              ATCAGCAGCCTGCAGTCTGAAGATTTTGCAGTTTATTACTGTCAGCAGTACAATAACTGG
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Method of improving the yield of heterologous Streptomyces lividans Patent: US 5223418-A 1 29-JUN-1993; Location/Qualifiers Arcuri,E.J., Brawner,M.E., Donovan,M.J., Keller,J.A. Gerber, R.G. proteins produced á

GCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAAAAAAGGGGGATACAGTGGAACTGACC GACTCAAGAAGAAGCCTTTGGGACCAAGGAAACTTCCCCCCTGATCATCAAGAATCTTAAG TGTACAGCTTCCCAGAAGAAGAAGAATAACAATTCCACTGGAAAAACTCCAACCAGATAAAG GACTCAAGAAGACCTTTGGGACCAAGGAAACTTCCCCCTGATCATCAAGAATCTTAAG GCAGCCACTCAGGGAAAGAAGTGGTGCTGGGCAAAAAAGGGGGATACAGTGGAACTGACC TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCAACCAGATAAAG Score 625; DB 6; Pred. No. 1.3e-134; 0; Mismatches 15; Length 1213; Indels <u>,</u> Gaps 120 138 60 378 300 318 240 258 180 198

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AX100880
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Eukaryota; Metazoa;
Mammalia; Eutheria;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spr identification of inhibitors of receptor-ligand interactions Patent: WO 0122084-A 30 29-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Jakobsen, B.K.
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GCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAAAAAAAGGGGATACAGTGGAACTGACC
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FQKTCSPI"
                                                                                                                                                                                                                                                                                                                                                                            /note="unnamed protein product"
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AR380468
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Cocks, B.G., Stuart, S.G. and Seilhamer, J.
Compositions for the detection of blood
                                                                                                                                                                                                                                                               response gene expression
Patent: US 6607879-A 1013 19-AUG-2003;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                      Unknown
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Pred. No. 1.8e-134;
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                                                                                   GTGCTAGCTTTCCAGAAGGCCTCCGG
                                                                                                                                                           ACCTGGACATGCACTGTCTTGCAGAACCAGAAGGAAGGTGGAGTTCAAAATAGACATCGTG
                                                                                                                                                                                                    AAAAACATACAGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC
                                                                                                                                                                                                                                    AAAAACATACAGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC
                                                                                                                                                                                                                                                                                                           CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT
                                                                                                                                                                                                                                                                                                                                        CTAGTGTTCGGATTGACTGCCAACTCTGACACCCCACCTGCTTCAGGGGCAGAGCCTGACC
                                                                                                                                                                                                                                                                                                                                                                               CTAGTGTTCGGATTGACTGCCAACTCTGACACCCCACCTGCTTCAGGGGCAGAGCCTGACC
                                                                                                                                                                                                                                                                                                                                                                                                               ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGTGCAATTG
                                                                                                                                                                                                                                                                                                                                                                                                                                   ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGTGCAATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCAACCAGATAAAG
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                                                                                                                                    ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
                                                                                                                                                                                                                                                                      CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT
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QKKSIQFHKKNSKQIKLGKGGSFLTKGPSKLANDASRRSLMPQGNFPLIIKNLKIE
DSDTYLCEVEDQKEEVQLLVFGLTANSDTHLLQCQGSLTITLBSPPGSSSVQCRSFRG
KNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKUEGQ
KNIQGGKKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKUTQDFKLQMGK
VEFSFPLAFTVEKLTGSGELMWQAERASSSKSWITFDLKNKEVSVKRVTQDFKLQMGK
KLPLHLTLPQALPQYAGSGNLTLLEAKTGKLHQEVNLVMATQLQKNLTCEVWGFT
SPKLMLSIKLENKEKKVKREKAVWYLMPEAGMWQCLLSDSGQVLLESNIKVLFTWST
SPKLMLSIKLENKEKKVKREKAVWYLMPEAGMWQCLLSDSGQVLLESNIKVLFTWST
SPKLMLSIKLENKEKKVKREKAVWYLMPEAGMWQCLLSDSGQVLLESNIKVLFTWST
SPKLMLSIKLENKEKTCQCPHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="T4 surface glycoprotein signal peptide"
151. .1449
/product="T4 surface glycoprotein mature peptide"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /protein_id="AAA35572.1"
/db_xref="GI:179142"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              note="T4 surface glycoprotein precursor"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /mol_type="mRNA"
/db_xref="taxon:9606"
76_1452
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Score 624.4;
Pred. No. 1.8e
0; Mismatches
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                                                                   701
                                                                                                   626
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                                                                                                                                                                                                                                                                                                        Query Match
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Matches 625
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1 (bases 1 to 1742)

2 (bases 1 to 1742)

2 (bases 1 to 1742)

3 (bases 1 to 1742)

3 (bases 1 to 1742)

4 (bases 1 to 1742)

5 (bases 1 to 1742)

6 (bases 1 to 1742)

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8 (bases 1 to 1742)

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Human 7
M35160
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             91216786
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                                                                                                                                                                                                                                                                                                                                        Similarity
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TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCAACCAGATAAAG 180
                                                                                                                GCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAAAAAAAGGGGGATACAGTGGAACTGACC 120
                                                                                                                                                                                    ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA
                                                             GCAGCCACTCAGGGAAAAGTGGTGCTGGGCAAAAAAGGGGATACAGTGGAACTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cytosine to thymidine transition at nucleotide position sults in substitution of TRP-240 for ARG-240.
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                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Immunol. 30 (2),
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T4 surface glycoprotein CD4 gene,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /translation="mingvpfrhlllvlqlallpaatqgkkvvlgkkgdtveltctas
gkks1qpfhwknsnutkilgnqgsfltkgpsklindradsrrslmdqgnfpliiknlkie
gkks1qpfhwknsnutkilgnqgsfltkgpsklindradsrrslmdqgnfpliiknlkie
gbtyt cevedqkebvqllvfgjtansdthllqqqsltitlespfgsspsvqcrsprg
kniqgkkteisvsqlelqdsgtmtctvlqnqkkvefkildvvlafqkasivykkegek
klplhltlpqalpqyagsgnltlaleaktgklhqevnlvvmratqlqknltcevwgpt
spklmislklenkeakvskrekavwvlnpeaqmwqcllsdsqvllesnikvlptwst
spklmislklenkeakvskrekavwvlnpeaqmwqcllsdsqvllesnikvlptwst
                                                                                                                                                                                                                                                                                                                                                                                                                                                            /gene="CD4"
/note="g in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FOKTCSP:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PVQPMALIVLGGVAGLLLFIGLGIFFCVRCRHRRRQAERMSQIKRLLSEKKTCQCPHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /codon_start=1
/protein_id="AAA16069.1"
/db_xref="GI:179144"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         product="T4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /gene="CD4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="T4 surface
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                gene="CD4"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          76. .1452
/gene="CD4"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /haplotype="OKT4-negative"
76. .1452
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="Homo sapiens"
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                                                                                                                                                                                                                                                                                                                                 43.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      .1449
                                                                                                                                                                                                                                                                                                                                                                                                                                                               in OKT4 epitope deficiency;
                                                                                                                                                                                                                                                                                                           0
                                                                                                                                                                                                                                                                                                                                 Score 624.4; DB 9;
Pred. No. 1.8e-134;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            surface
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                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       glycoprotein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glycoprotein mature peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       signal peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             precursor"
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                                                                                                                                                                                                                                                                                                                                                                  Length 1742;
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30333 USA
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Patent: EP 0325262-A2 3 26-JUL-1989,
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                                                                                                              ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGAGGTGCAATTG
                                     TGTACAGCTTCCCAGAAGAAGAAGAATACAATTCCACTGGAAAAAACTCCAACCAGATAAAG
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/mol_type="unassigned
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1 (bases 1 to 3133)
Brian,S.D.
Broned genes encoding IG-CD4 fusion Cloned genes encoding IG-CD4 fusion Patent: EP 0325262-A2 1 26-JUL-1989;
Patent: Location/Qualifiers
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Sequence 1 from Patent
IO8115
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A baculovirus expression system for magnetic sorting of infected cells and enhanced titer determination
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                                                                                                                                                                                                                                                                                                                                                                                                                                               other sequences; artificial sequences; 1 (bases 1 to 7533)
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/gene="CD4-EGFP"
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VTAAGITLGMDELYK"
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/transl_table=11
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12; Length 7533;

Local Similarity 99.0 GACTCAAGAAGAAGCCTTTGGGACCAAGGAAACTTCCCCCCTGATCATCAAGAATCTTAAG GCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAAAAAAAGGGGGATACAGTGGAACTGACC ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGTGCAATTG TGTACAGCTTCCCAGAAGAAGAAGAACATTACAATTCCACTGGAAAAAACTCCAACCAGATAAAAG GCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAAAAAAAGGGGGATACAGTGGAACTGACC CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT CTAGTGTTCGGATTGACTGCCAACTCTGACACCCACCTGCTTCAGGGGGCAGAGCCTGACC CTAGTGTTCGGATTGACTGCCAACTCTGACACCCACCTGCTTCAGGGGCAGAGCCTGACC ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGTGCAATTG GACTCAAGAAGCCTTTGGGACCAAGGAAACTTCCCCCTGATCATCAAGAATCTTAAG TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCAACCAGATAAAG 43.48; Score 624.4; DB 12 Pred. No. 1.7e-134; 0; Mismatches 1; Indels 0, Gaps 5915 5975 6035 6095 6155 6215 6275 6335 540 480 420 360 300 240 180 120 60 0

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1 (bases 1 to 1273)

Deen,K.C., Folena-Wasserman,G.M., Inc
Process for purification of soluble 7

Protess for purification 26-APR-1989;

Patent: EP 0313377-A1 1 26-APR-1989;

Location/Qualifiers
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                        ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
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Arthos, J., Clark, P.E., Fornwald, J.A., Brawner, M.E., Gorman, J.A., Sathe, G.M., Sweet, R.W. and Taylor, D.P. Expression of HIV binding proteins Patent: EP 0331356-A2 1 06-SEP-1989;
Locatin/Qualifiers
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Unclassified.
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Unclassified.
1 (bases 1 to 1304)
E 1 (bases 1 to 1304)
S Seed, B., Banapour, B., Romeo, C. and Kolanus, W.
Targeted cytolysis of HIV-infected cells by chir
receptor bearing cells
receptor bearing cells
Location/Qualifiers
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AR067943.1 GI:5999165
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          GTGCTAGCTTTCCAGAAGGCCTCCGG 626
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                                                                                               AAAAACATACAGGGGGGGAAGACCCTCTCCGTGTCTCAGCCTGGAGCTCCAGGATAGTGGC
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GTGCTAGCTTTCCAGAAGGCCTCCAG 736
                                          ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
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RESULT

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RESULT 15 AR560088 LOCUS DEFINITION	D ₀ Qy	gb Qy	D Qy	Qy db	Db Qy	Db Qy	gb Qy	Qy db	Db Qy	D Qy	D Q	Query Ma Best Loc Matches	ORIGIN	NAL	SOURCE ORGANISM REFERENCE	AR166802 LOCUS DEFINITION ACCESSION VERSION KEYWORDS
AR560088 1304 bp mRNA linear PAT 08-OCT-2004 Sequence 28 from patent US 6753162.	601 GTGCTAGCTTTCCAGAAGGCCTCCGG 626 	541 ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG 600 	481 AAAAACATACAGGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC 540	421 CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT 480	361 CTAGTGTTCGGATTGACTGCCAACTCTGACACCCACCTGCTTCAGGGGCAGAGCCTGACC 420	301 ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGAGGTGCAATTG 360 	241 GACTCAAGAAGAAGCCTTTGGGACCAAGGAAACTTCCCCCCTGATCATCAAGAATCTTAAG 300 	181 ATTCTGGGAAATCAGGGCTCCTTCTTAACTAAAGGTCCATCCA	121 TGTACAGCTTCCCAGAAGAAGAGGACATACAATTCCACTGGAAAAACTCCAACCAGATAAAG 180 	61 GCAGCCACTCAGGGAAAGTAGTGGTGGTGCAAAAAAGGGGATACAGTGGAACTGACC 120	1 ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA 60	al 6	Œ) MH 11 (0	Unknown. Unknown. Unclassified. 1 (bases 1 to 1304)	AR166802 1304 bp DNA linear PAT 17-OCT-2001 Sequence 28 from patent US 6284240. AR166802 AR166802.1 GI:16243143

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ACCESSION
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KEYWORDS
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Unclassified.

1 (bases 1 to 1304)

1 (bases 1 to 1304)

Seed, B., Banapour, B., Romeo, C. and Kolanus, W.

Targeted cytolysis of HIV-infected cells by chimeric CD4

receptor-bearing cells

Patent: US 6753162-A 28 22 JUN-2004;
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AR560088.1
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ilarity 99.7%;
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/mol_type="mRNA"
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9866.236 Million cell updates/sec
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

43.4 1742 11 43.4 1910 3 A 43.4 1910 3 A 43.4 1910 3 A	43.4 1742 11 43.4 1910 3 A 43.4 1910 3 A	43.4 1742 11 43.4 1910 3 A	43.4 1742 11	43 4 1742 11		15 624.4 43.4 1742 11 ADI31687		43.4	43.4	43.4	43.4	43.4	43.4			5 624.4 43.4 1419 10 ADA44806	4 624.4 43.4 1415 2 AAQ38761	3 624.4 43.4 1377 4 AAF82582	2 625 43.4 8911 12 ADN07735	1 1440 100.0 1440 3 AAA54045	Result Query No. Score Match Length DB ID
	Aaz48204 DNA secue	Aaz44064 Human fus	Adabu663 UNA encod		Abd20870 Human pul	Adi31687 Human cDN	Abz97021 Human nuc	Aai65462 Nucleotid	Aaf21327 Human low	Aaa35205 Human ade	Aaz48203 DNA seque	Aaz44063 Human fus	Aaa50662 DNA encod	Aaq38759 sCD4-HAP	Aaq38760 sCD4-L1 l	Ada44806 CD4/TCR C	Aaq38761 sCD4-L2 l	Aaf82582 Human CD4	Adn07735 Expressio	Aaa54045 sCD4-SCFv	Description

Novel neutralizing bispecific fusion proteins effective in viral such as

ALIGNMENTS

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ID AAA54
XX AAA54
XX AAA5
XX AAA5
XX Fusi
CH SCD4
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                                                                     WPI; 2000-638183/61.
P-PSDB; AAB00158.
                                                                                                                                                                                                                                                                                                                                                                                                                              16-MAR-2000; 2000WO-US006946.
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/product= "This sequence does not fully encode the cross referenced protein given in GENESEQ record AAB00158. protein sequence also comprises a 28 amino acid C-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            terminal peptide"
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Best Local Similarity
Matches 1440; Conserv
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standard; DNA; ВP

15-JUL-2004 (first entry)

Expression vector DNA

Immunogenic complex; gp120; CD4; HIV; HIV infection; anti-HIV; circular; cyclic; ds.

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Best Local Similarity
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06-MAY-1994;
20-DEC-1995;
11-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to an immunogenic complex comprising gp120 covalently bonded to a CD4 equivalent molecule, fragment of CD4 or its equivalent. The invention also relates to a composition comprising the complex and a carrier, an antibody reactive with the complex, an immortalised cell line that produces the complex, a method of detecting the HIV antigen in a test fluid, involving contacting the test fluid with an antibody raised against the immunogenic complex and detecting the presence of immune complexes formed between the antigen in the test fluid and the antibody, and a vaccine comprising an immunogenically effective amount of the immunogenic complex. The immunogenic complex is useful for raising neutralising antibodies against HIV, which involves administering the complex to a subject in a carrier, and for treating HIV infections.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Immunogenic complex, covalently bonded to
                                                                                                                                                                                                                                                                                                                                              Sequence 8911 BP; 2188 A; 2221 C; 2227 G;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; SEQ ID NO 3; 26pp; English.
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17-JUL-2001;
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98US-00075544.
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                                                                                                                                                                                                                                                                                                                   43.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Human; CD4; T4; CD4 fusion protein; oligomerisation; receptor-ligand interaction inhibition; surface plasmon resonance; SPR; T cell receptor binding; MHC binding; carcinoma; autoimmune disease; multiple sclerosis; human immunodeficiency virus; HIV; diabetes; rheumatoid arthritis; immune disorder; ss.
                                                                                             Sequential screening of candidate compounds library for the inhibit binding of low affinity receptor-ligand interaction binding kinetics, using interfacial optical assay.
                                                   Disclosure;
                                                                                                                                                                                                     P-PSDB;
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present sequence encodes human

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Human CD4 extracellular domains

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       proteins. The fusion proteins contain an oligomerisation domain that enables the proteins to bind to one another to form oligomers. The oligomers may be used in an invention relating to a method for screening for compounds with the ability to inhibit a low affinity receptor-ligand interaction. The method uses an interfacial optical assay, such as surface plasmon resonance (SPR). The method is useful for screening candidate compounds for the ability to inhibit interaction between MHC/peptide complex and T cell receptor, and MHC/peptide complex and CD8 or CD4 co-receptor. The compounds identified by the above methods which interfere with T cell receptor binding to a particular HLA type molecule are useful as immune inhibitors for treating carcinomas, autoimmune diseases such as multiple sclerosis, human immunodeficiency virus (HIV) infection, rheumatoid arthritis, Hashimoto's disease, insulin dependent
           AAQ38761;
                                     AAQ38761 standard; DNA; 1415
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99.8%;
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Pred. No. 1.7e-129;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New fusion protein used in gene therapy for treating AIDS - comprises protein which binds to retroviral envelope protein which targets fusion protein to lysosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Soluble CD4; HIV; Human immunodeficiency Virus; envelope; glycoprotein; polymerase chain reaction; lysosomal membrane protein; lamp-2; ss.
                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1415 BP; 360 A; 365
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Primers P-1 and P-2 (AAQ38748 and AAQ38749) were used to amplify
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                        Composition for treating or preventing human immune deficiency virus, comprises CD4 chimeric protein having a protective effect in trans, c related nucleic acid.
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T cell receptor CD3epsilon chain; C-terminal domain; CD4epsilon15;
gene therapy; human; gene; ds.
                                                                                                                                                                                                        Alarcon Sanchez BJ,
Gomez Buendia M;
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DB; ADA44807.
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/partial
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/note= "No stop codon given"
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Claim 5; Page
                             31-33; 43pp;
                             Spanish
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CC compositions of the invention have been transduced with a vector that encodes comparises CD4+ cells that have been transduced with a vector that encodes condoplasmic reticulum (ER). The invention also encompasses the use of a cC soluble protein factor produced by CD4+ cells that have been transduced cC with a vector encoding a chimeric CD4 protein; and the use of an CC expression system encoding a chimeric CD4 protein. The ER-localised CC chimeric CD4 molecule binds to the HIV-1 envelope protein gp160, CC resulting in HIV-1 retention in the ER and thereby preventing viral CC replication. In a specific embodiment, the chimeric CD4 molecule CC comprises CD4 fused to 15 amino acids of the C-terminal domain of the TC cell receptor CD3epsilon chain; this chimeric CD4 molecule is designated CC CD4epsilon15 (ADA44807). A known chimeric CD4 of similar structure but CC compositions of the invention have an in trans effect on the replication CC HIV-1, and may be used to treat and prevent HIV-1 infection. The CC consecution is specifically claimed for use in compositions of the invention and prevent HIV-1 infection. The CC chaepsilon15, which is specifically claimed for use in compositions of the invention. The invention relates to a composition for the treatment or prevention of human immunodeficiency virus-1 (HIV-1) infection. The composition

Sequence 1419 BP; 362 A; 367 C; 405 G. 285 T; 0 U; 0 Other;

Ş 밁 g 밁 Š 밁 Ś 밁 밁 Ş 뮹 Ş 5 Ś 밁 S g δ δ 밁 δ Matches Query Match Local 601 541 541 481 481 421 421 361 361 301 301 241 241 181 181 121 121 625; 61 61 1 ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA \vdash Similarity GACTCAAGAAGAAGCCTTTGGGACCAAGGAAACTTCCCCCTGATCATCAAGAATCTTAAG GACTCAAGAAGAAGCCTTTGGGACCAAGGAAACTTCCCCCTGATCATCAAGAATCTTAAG TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCAACCAGATAAAG GTGCTAGCTTTCCAGAAGGCCTCCGG CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT CTAGTGTTCGGATTGACTGCCAACTCTGACACCCACCTGCTTCAGGGGCAGAGCCTGACC ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGTGCAATTG TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCAACCAGATAAAG GCAGCCACTCAGGGAAAGAAGTGGTGCTGGGCAAAAAAGGGGGATACAGTGGAACTGACC ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG AAAAACATACAGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC AAAAACATACAGGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC CTGACCTTGGAGAGCCCCCCCTGGTAGTAGCCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT CTAGTGTTCGGATTGACTGCCAACTCTGACACCCACCTGCTTCAGGGGCAGAGCCTGACC ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGTGCAATTG Conservative 43.4%; 0; Mismatches Score 624.4; DB 10 Pred. No. 1.8e-129; 626 DB 10; Indels Length 1419; 0 Gaps 600 600 540 540 480 480 420 420 360 360 300 300 240 240 180 180 120 120 60 60 0

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                protein
protein
  09-JAN-2001
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                                                     AAA50662;
                                                                                                        AAA50662
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                                                                                                        standard;
                                                                                                                                                                                                                                                                              GTGCTAGCTTTCCAGAAGGCCTCCGG
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  (first entry)
                                                                                                        DNA; 1714
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Pred. No. 1.8e-129;
0; Mismatches 1;
                                                                                                        ВP
                                                                                                                                                                                                                                                                                               626
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22-JAN-1988;
23-JAN-1989;
09-JUN-1992;
12-APR-1993;
                                                                                                      CD4-immunoglobulin
                                                                                                                                                                                   07-JUN-1995;
                                                                                                                                                                                                                                  exon
                                                                                                                                                                                                                                                                     CDS
                                                                                                                                                                                                                                                                                          Key
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                                                                                                                                                    04-FEB-1994;
                                                                                                                                                                                             12-SEP-2000
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                                                                                                                                                                                                                                                                                    exon
                                                                                                                                                                                                                                                                                                   Homo sapiens
                                                                                                                                          (GEHO)
                                                                                                                                                                                                                                                                                                                            encoding
                                                                                                                     2000-586558/55
                                                                                       ۲,
                                                                                                                 AAB19509
                                                                                                                                          GEN
                                                                                                                                                                                                                                                                                                             diagnosis;
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                                                                                                                                          HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                            CD4-IgM fusion
                                                                                      41-50; 39pp; English.
                                                                                                                                                         88US-00147351.
89US-00299596.
92US-00896781.
93US-00057952.
                                                                                                                                                    94US-00191708
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                                                                                                                                                                                                                     /number= 1
1665. .1714
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111. .1714
                                                                                                                                                                                                                                                                                    Location/Qualifiers
                                                                                                                                                                                                                                                                                                                  CD4Mmu;
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                                                                                                                                                                                                                                               note= "contains
309. .1664
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                                                                                                      fusion
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                                                                                                                                                                                                                                                                                                                   fusion
                                                                                                      proteins, useful for targeting
                                                                                                                                                                                                                                                                                                                             protein CH4Mmu.
                                                                                                                                                                                                                                                                                                                  protein; immunoglobulin; HIV; SIV;
                                                                                                                                                                                                                                                      an
                                                                                                                                                                                                                                                      intron"
                                                                                                      gp120 of HIV
                                                                                                                                                                                                                                                                                                                  gp120;
                                                                                                       or
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The present sequence is that of DNA encoding fusion protein CD4Mmu (see CAAB19509) comprising the extracellular portion of CD4, which binds to HIV gpl20, linked at its C-terminus to a human IgM heavy chain polypeptide. To obtain the construct, DNA encoding CD4 was linked to IgM DNA at the Mst2 site upstream of the CH1 region. A plasmid containing this genetic construct is deposited in Escherichia coli MC1061/P3 as ATCC 67609. This in protein CD4Mmu and a nucleic acid encoding it are claimed. Also claimed are a vector comprising the nucleic acid, and a method of producing the fusion protein in secreted form using a transformed host cell. The fusion protein may further comprise a therapeutic agent, radiolabel or NMR imaging agent. The fusion protein can be administered to an animal (including humans) for treatment of HIV or SIV infection, and can also be used in assays for HIV or SIV, imaging and tissue stains. If IgM fusion proteins such as CD4Mmu provide complement-mediated immunity NIV, imaging and tissue stains. complement-mediated immunity (see

á 밁

ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA

ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA

170 60

111

Query Match Best Local Matches

Similarity

43.4%;

624.4; DB 3; No. 1.8e-129;

Length 1714;

0,

Gaps

0

0

Mismatches

Sequence

1714 BP; 411 A; 503

Ç Score Pred. 467

<u>ن</u>

333 T; 0 U; 0 Other;

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RESULT 9
AAZ44063
ID AAZ4
XX AAZ4
XX AAZ4
XX AAZ4
XX Pusi
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XX Homc
OS Synt
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23-JAN-1989;
09-JUN-1992;
12-APR-1993;
    HPI;
                                             Seed
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                                                                                                                                                                                                                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                         Fusion protein; anti-human immum
                                                                                                                                                                                                                                    04-FEB-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Human fusion
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                                                                                                                                                                                                                                                                                                                                                                                                                         tein; human; CD4; IgM; immunoglobulin; gp120;
immunodeficiency virus; CD4Mg; ds.
                                                                                       HOSPITAL
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                                                                                                                              88US-00147351.
89US-00299596.
92US-00896781.
93US-00057952.
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RESULT 10
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Matches 625
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1714 BP; 411 A; 503 C; 467
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GTGCTAGCTTTCCAGAAGGCCTCCGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAAAAAAGGGGGATACAGTGGAACTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAAAAAAAGGGGGATACAGTGGAACTGACC
                                                      ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
                                                                                                           AAAAACATACAGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC
                                                                                                                                             CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT
                                                                                                                                                                 CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT
                                                                                                                                                                                                     CTAGTGTTCGGATTGACCACCCACCTGCTTCAGGGGCAGAGCCTGACC
                                                                                                                                                                                                                                                                                                                  GACTCAAGAAGCCTTTGGGACCAAGGAAACTTCCCCCTGATCATCAAGAATCTTAAG
                                                                                                                                                                                                                                                                                                                                                                      TGTACAGCTTCCCAGAAGAAGAACATACAATTCCACTGGAAAAACTCCAACCAGATAAAG
                                      ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
                                                                                            AAAAACATACAGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC
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Pred. No. 1.8e-129;
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14-MAR-2000

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Matches 625
                                                                                                                                                                                                                                                                                                                                                                                                                     comprises an extracellular CD4 DNA sequence or its fragment which binds to HIV gp120 when fused to an immunoglobulin (Ig) chain and the DNA sequence of an Ig heavy or light chain, where the DNA sequence encoding the variable region has been replaced with the DNA sequence which encodes extracellular CD4 or its gp120 binding fragment. The fusion protein is capable of being secreted. The fusion proteins are useful for treating HIV or SIV infections in animals, preferably humans. They are also useful for producing medicaments which can be used for treating HIV or SIV infections in humans. The present sequence represents the DNA which encodes the fusion protein CD4Mmu where the CD4 is linked to human IgG1
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                                                                                                                                                                                                                                                                                                                                                                               Sequence 1714 BP; 411 A; 503 C; 467 G; 333 T;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New fusion gene encoding immunoglobulin-CD4 fusion proteins, useful the treatment of HIV or simian immunodeficiency virus infections.
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                                                                                                                                                                                                                                                                                                                                                                                                          the Mst2 site upstream of the CH1 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               invention provides a fusion gene encoding a fusion protein that
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DB; AAY59170.
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                                                                                                                                                                                                                                                                                                                                         Similarity
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                                                                                                                         TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCCAACCAGATAAAG
                                                                                                                                                                                                                 GCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAAAAAAAGGGGATACAGTGGAACTGACC
                                                                                                                                                                                                                                 GCAGCCACTCAGGGAAAGAAGTGGTGCTGGGCAAAAAAAGGGGGATACAGTGGAACTGACC
                                                                                                                                                                                                                                                                      ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA
                                                                                                                                                                                                                                                                                        ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCCCA
                  ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGTGCAATTG
                                                                              GACTCAAGAAGCCTTTGGGACCAAGGAAACTTCCCCCTGATCATCAAGAATCTTAAG
                                                                                                                                                            TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCAACCAGATAAAG
                                                                                                       Page 47-53;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HOSPITAL CORP
                                                                                                                                                                                                                                                                                                                          Conservative
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Pred. No. 1.8e-129;
0; Mismatches 1;
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                                                                                                                      AAAAACATACAGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC
                                                                                                                                                                                                                          CTAGTGTTCGGATTGACTGCCAACTCTGACACCCACCTGCTTCAGGGGCAGAGCCTGACC
                                                                      ACCTGGACATGCACTGTCTTGCAGAAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
                                                                                                                                                        CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT
                                                                                                                                                                                                           CTAGTGTTCGGATTGACTGCCAACTCTGACACCCCACCTGCTTCAGGGGCAGAGCCTGACC
 GTGCTAGCTTTCCAGAAGGCCTCCAG
                         GTGCTAGCTTTCCAGAAGGCCTCCGG
                                                   ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
                                                                                                      AAAAACATACAGGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC
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AAA35205 standard; DNA; 1742 ВP

28-JUL-2000

(first

Human adenosine receptor related polynucleotide 2nd SEQ ID NO:79.

RESULT 11
RABA35205
ID ARA35
XX ARA35
X Human; adenosine receptor; low adenosine antisense oligonucleotide; phosphorothioate; impaired respiration; infilammation; allergy; allergic disease; bronchoconstriction; inhibitor; antinflammatory; antiallergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthma; respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD; cancer; leukaemia; lymphoma; carcinoma; metastasis; ss.

Homo sapiens.

WO200009525-A2

24-FEB-2000

03-AUG-1999; 99WO-US017712.

03-AUG-1998; 98US-0095212P

(UYEC-) UNIV EAST CAROLINA

2000-205971/18

New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstruction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia or

Disclosure; Page 1245; 1343pp; English

The present invention describes a new composition comprising an antisense oligonuclectide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions are useful for the treatment of diseases associated with inflammation, impaired already, including lung diseases and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating e.g. ischaemic conditions, pulmonary vasconstriction, allergies, asthma, e.g. ischaemic conditions, pulmonary vasconstriction, allergies, asthma, impeded respiration, respiratory distress syndrome, pain,

14-MAR-2001

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 1742 BP; 405 A; 492 C; 466 G; 379 T; 0 U; 0 Other;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              61 GCAGCCACTCAGGGAAAGAAGTGGTGCTGGGCAAAAAAAGGGGATACAGTGGAACTGACC
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GTGCTAGCTTTCCAGAAGGCCTCCGG 626
                                                                                                        ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
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                                                                             ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
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respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary hypertension; emphysema; pulmonary transplantation rejection; chronic obstructive pulmonary disease; pulmonary infection; bronchitis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammatory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic
                                                                                                                 06-APR-1999;
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Low adenosine (A) content antisense oli adenosine receptors during metabolism, and respiratory obstructions. oligonucleotides which do not trigger sm, useful e.g. for treating cancers

Page 1329; 1592pp; English.

CC immunosuppressive, antiasthmatic, hypotensive and cytostatic activities.

CC The antisense oligonucleotides and (I) can be used to down-regulate the CC expression and or activity of target polypeptides associated with CC lung/respiratory disorders and malignancies, such as stimulating and activating peptide factors and transmitters, transcription factors, C immunoglobulins and antibodies, antibody receptors, cytokines and cchemokines, endogenously produced specific and non-specific enzymes, C binding proteins, adhesion molecules and their receptors, cytokine and CC chemokines receptors, adenosine receptors, bradykinin receptors, central nervous system peptide receptors, brinding proteins and peripheral nervous and non-nervous system peptide cransmitters, defensins, growth factors, vasoactive peptides and creceptors, brinding proteins and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders including respiratory obstruction (especially pulmonary obstruction and/or lung inflammation, allergy(ies) and/or surfactant hypoproduction which are associated with a disease or condition selected from pulmonary vasoconstriction, allergies, asthma, impeded respiratory distress syndrome (RDS), pain, cystic fibrosis (CF), allergic rhinitis (AR), pulmonary conduction, and/or listress syndrome, conduction, pulmonary infections, bronchitis, and/or cancer. AAF18434 to AAF21543 represent human polynucleotide fromention of the present invention of The present invention describes low adenosine (A) content antisense oligonucleotides and compositions (I) comprising them. In the antisense oligonucleotides the A is replaced by a 'Universal' or alternative base. (I) can have respiratory, bronchodilator, antiinflammatory, analgesic, (I) can have respiratory, bronchodilator, antiinflammatory, analgesic,

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AAF21327

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Query Match Best Local Sir Matches 625; Similarity 43.4%; ilarity 99.8%; Conservative 0 Score 624.4; DB Pred. No. 1.8e-1; 0; Mismatches .8e-129 ω -. Length 1742; 0 Gaps 0,

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An antibody for the treatment or prevention of HIV-infection comprises gp120 portion which binds to DC-SIGN or is exposed upon gp120 binding of DC-SIGN due to concomitant conformational change.
                                                                                                                                                                   WPI; 2001-602565/68
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Disclosure; Page 121-122; 131pp; English

The specification describes an antibody which is specific for an antigenic fragment of gpl20. This antigenic fragment binds to DC-SIGN or is exposed upon gpl20 binding of DC-SIGN due to concomitant conformational change. DC-SIGN is a receptor that is specifically expressed on dendritic cells and facilitates infection of T lymphocytes with HIV. DC-SIGN is identical to a HIV-1 gpl20-binding C-type lectin. DC-SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes) with high affinity. The antibody of the invention inhibits the trans enhancement of HIV entry into a T cell or macrophage facilitated by dendritic cells. The antibody is useful to treat or prevent HIV infection. The present sequence represents a human polynucleotide, which is used in the course of the invention g

Sequence 1742 BP; 405 A; 491 C; 466 G; 380 T; 0 U; 0 Other;

5 δ Ś Ş S S 뭐 Ş Вb δ 밁 δ Дb δ 밁 멍 밁 밁 밁 밁 S Query Match Best Local S Matches 301 676 601 616 541 556 481 496 421 436 361 376 316 241 256 181 196 121 136 625; 61 GCAGCCACTCAGGGAAAGAAAGTGGTGGTGGGCAAAAAAAGGGGGATACAGTGGAACTGACC 76 1 ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA Similarity AAAAACATACAGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGTGCAATTG GACTCAAGAAGAAGCCTTTGGGACCAAGGAAACTTCCCCCCTGATCATCAAGAATCTTAAG GTGCTAGCTTTCCAGAAGGCCTCCGG ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT CTAGTGTTCGGATTGACTGCCAACTCTGACACCCACCTGCTTCAGGGGCAGAGCCTGACC CTAGTGTTCGGATTGACTGCCAACTCTGACACCCCACCTGCTTCAGGGGCAGAGCCCTGACC ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGTGCAATTG TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCAACCAGATAAAG GCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAAAAAAAGGGGGATACAGTGGAACTGACC ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA GTGCTAGCTTTCCAGAAGGCCTCCAG ACCTGGACATGCACTGTCTTGCAGAACCAGAAGGAAGGTGGAGTTCAAAATAGACATCGTG AAAAACATACAGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT GACTCAAGAAGAAGCCTTTGGGACCAAGGAAACTTCCCCCCTGATCATCAAGAATCTTAAG TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCAACCAGATAAAG Conservative 43.4%; 0; Mismatches Score 624.4; DB 4; Pred. No. 1.8e-129; 0; Mismatches 1; 701 626 Indels Length 0, Gaps 600 615 540 555 480 495 420 435 360 375 300 315 240 255 180 195 120 135 60

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                                                                                                                                             Query Match
Best Local Similarity
Matches 625; Conserv
                                                                                                                                                                                                                                                                                       specification, at ftp.wino in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy; antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
                                                                                                                                                                                                                                          Sequence 1742 BP; 405
                                                                                                                                                                                                                                                                                                          lung surfactant in a subject's tissue, or treating bronchoconstriction, lung inflammation, lung allergies, or a respiratory disease or condition. Note: The sequence data for this patent is not represented in the printed specification, but was obtained in electronic format directly from WIPO
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                                                   WPI; 2003-895307/82
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condition,

altered expression of genes in an immunological response or for diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma or osteoarthritis. Claim 1; SEQ ID NO 1013; 50pp; English

CC hybridisation complexes with the level of hybridisation complexes with the level of hybridisation complexes with the level of hybridisation complexes correlates with the presence of the detected comprising in a mon-diseased sample, where an altered level of the detected hybridisation complexes correlates with the presence of an comprising a microarray and a plurality of detectable complexes and a comprising a microarray and a plurality of polynucleotide probes. The cDNAs compression of target polynurality of polynucleotide probes. The cDNAs complexes of an immunopathology, such as Crohn's disease, asthma, confidentifying a plurality of polynucleotide probes. The cDNAs confidentifying a plurality of polynucleotide probes. The cDNAs confidentifying agents for the treatment of the diseases, asthma, consecutive colitis, hypereosinophilia, irritable bowel syndrome, confidentifying agents for the treatment of the diseases. The microarray may consist on the diseases of an drug discovery and development, toxicological and consecutive studies, forensics or pharmacogenomics. The composition consecution of a subpopulation of mRNAs, cDNAs or consecution. Note: The sequence represents a human cDNA of the composition of the printed specification but was obtained in electronic format directly consecutive and secution but was obtained in electronic format directly are consecutive. The invention relates to a composition comprising a plurality of cDNAs for detecting the altered expression of genes in an immunological response. The invention also relates to a method of diagnosing or monitoring the treatment of an immunopathological condition in a sample, comprising obtaining nucleic acids from a sample, contacting the nucleic acids of the sample with an array comprising the plurality of cDNAs under conditions to form one or more hybridisation complexes, detecting the USPTO at seqdata.uspto.gov/sequence.html. under

Sequence 1742 BP; 405 A; 491 C; 466 G; 380 T; 0 U; 0 Other;

Query Match Best Local (Matches 625; 196 136 181 121 61 76 ш Similarity TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCAACCAGATAAAG 180 GCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAAAAAAGGGGATACAGTGGAACTGACC 120 ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCCTA 60 GCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAAAAAAAGGGGATACAGTGGAACTGACC ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA TGTACAGCTTCCCAGAAGAAGAAGCATACAATTCCACTGGAAAAACTCCAACCAGATAAAG Conservative 43.4%; Mismatches Score 624.4; DB 11; Length 1742; Pred. No. 1.8e-129; <u>ب</u> Indels 0 Gaps 135 195 255 0

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ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGAGGAGGAGGAGGAGGTGCAATTG 360 GACTCAAGAAGAAGCCTTTGGGACCAAGGAAACTTCCCCCCTGATCATCAAGAATCTTAAG GACTCAAGAAGAGCCTTTGGGACCAAGGAAACTTCCCCCCTGATCATCAAGAATCTTAAG

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Search completed: September 20, 2005, 10:37:09 Job time : 870 secs

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Result
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US-09-518-3918-28
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US-08-284-3918-2
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AAGGGGT 480 AAGGGGT 558	C 42	GCAATTG 360 CAATTG 438	TCTTAAG 300 CTTAAG 378	TCGCGCT 240 TCGCGCT 318	GATAAAG 180 ATAAAG 258	ACTGACC 120 ACTGACC 198	CCTCCCA 60	Gaps 0;			e 1, Appli e 3, Appli e 8, Appli e 8, Appli e 5, Appli e 5, Appli e 1, Appli e 2, Appli e 2, Appli e 2, Appli e 2, Appli e 3, Appli e 6, Appli e 6, Appli e 6, Appli

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RESULT 2
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; TITLE OF INVENTION: METHOD OF IMPROVING THE YIELD OF INTITLE OF INVENTION: METHOD OF IMPROVING THE YIELD OF HETEROLOGOUS PRODUCED BY STREPTOMYCES LIVIDANS;
; MUMBER OF SEQUENCES: 2
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/589,979
; APPLICATION NUMBER: 28-SEP-1990
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                ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
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; Sequence 4, Application PC/1; GENERAL INFORMATION:
; APPLICANT: Tang, J. N.
; TITLE OF INVENTION: Fue:
; TITLE OF INVENTION: Aid;
; NUMBER OF SEQUENCES: 15
; CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRE1
TELECOMUNICATION INFORMATION:
TELEPHONE: 404-572-6508
TELEPAX: 404-572-6555
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1415 base pairs
TYPE: NUCLEIC ACID
TYPE: NUCLEIC ACID
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Best Local Similarity
Matches 625; Conserv
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NAME/KEY: misc_feature

'COATTON: 1410..1415

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NAME/KEY: misc_feature

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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08090
FILING DATE: 19920922
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,
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CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                     NAME/KEY: misc_feature LOCATION: 1275..1280 OTHER INFORMATION: /not
                                                                                                                                                                                                        LOCATION: 1410..14
OTHER INFORMATION:
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OTHER INFORMATION: /note=
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100 Peachtree Street
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                                                                                                                                                                                                          /note=
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                                                                                                                                          Score 624.4; DB 5;
Pred. No. 5.4e-138;
                                                                                                                                                                                                          "Restriction site"
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                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                        site"
                                                                                                                                                         DB 5;
                                                                                                                                                         Length 1415;
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RESULT 4
PCT-US92-08090-3
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GENERAL INFORWATION:
APPLICANT: Tang, J. N.
TITLE OF INVENTION: Fusion Proteinment of INVENTION: Aids
TELEFAX: 404-572-6555
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1421 base pairs
TYPE: NUCLEIC ACID
                                                                                                                                                                                                     ZIP: 30303
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPUTER: PSYSTEM: PC-DOS/MS-DOS
SOFTMARE: Patentin Release #1.0, V.
CURRENT APPLICATION DATA:
                                                                    ATTORNEY/AGENT INFORMATION:
NAME: PABSE, PALTES I.
REGISTRATION UNMBER: 31,284
REFERENCE/DOCKET NUMBER: OWRF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-572-6508
                                                                                                                                                                                                                                                                                                                                                TITLE OF INVEST. 15
NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
ADDRESSEE: NO Peachtree Street
                                                                                                                                                                                                                                                                                                        CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
                                                                                                                                                             APPLICATION NUMBER: POFILING DATE: 19920922 CLASSIFICATION:
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Best Local (
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HYPOTHETICAL: NO
ANTI-SENSE: NO
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ORIGINAL SOURCE:
ORGANISM: Homo sapien
TISSUE TYPE: Epithelial
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OTHER INFORMATION: /note=
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LOCATION: 1275..1280
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625; Conserv
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                GTGCTAGCTTTCCAGAAGGCCTCCGG
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                                                      ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
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Pred. No. 5.4e
0; Mismatches
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                           626
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5.4e-138;
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NAME: Pabst, Patrea L.

REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF.

TELECOMMUNICATION INFORMATION:

TELEPHONE: 404-572-6508
TELEPAX: 404-572-6555
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1448 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ORIGINAL SOURCE:
ORGANISM: Homo sapien
TISSUE TYPE: Epithelial
FEATURE:
                                                                                                                                                                                                                                                                                                                     Query Match
Best Local Similarity 99.8
Matches 625; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 2, Application PC/TUS9208090
GENERAL INFORMATION:
APPLICANT: Tang, J. N.
TITLE OF INVENTION: Fusion Protein Genes for Treatment of
TITLE OF INVENTION: Aids
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: PAC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION DATA:
APPLICATION UMBER: PCT/US92/08090
FILING DATE: 1920922
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
LOCATION: 1275..1280
OTHER INFORMATION: /note= "Restriction site"
FEATURE:
NAME/KEY: misc_feature
LOCATION: 1444..1448
OTHER INFORMATION: /note= "Restriction site"
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ADDRESSEE: Kilpatrick & Cody
STREET: 100 Peachtree Street
CITY: Atlanta
STATE: Georgia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: misc_feature
LOCATION: 1..6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       OTHER INFORMATION: /note= "Restriction site" FEATURE:
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TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCAACCAGATAAAG
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99.8%; Pred. No. 5.4e-138;
tive 0; Mismatches 1;
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QY 181 ATTCTGGGAAATCAGGGCTCCTTTAACTAAAGGTCCAAGCTGAATGATCGCGCT 240	a t
Db 196 TGTACAGCTTCCCAGAAGAAGAAGACATTCCACTGGAAAAAACTCCAACCAGATAAAG 255	U
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136 GCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAAAAAAGGGGATACAGTGGAACTGACC	, ט
1 GCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAAAAAAGGGGGATACAGTGGAACTGACC	0 5
135 136 137	
Query Match 43.4%; Score 624.4; DB 3; Length 1742; Best Local Similarity 99.8%; Pred. No. 5.7e-138; Matches 625; Conservative 0; Mismatches 1; Indels 0; Gaps)
; LENGTH: 1742 ; TYPE: DNA ; ORGANISM: Homo sapiens US-09-517-605-7	d
; CURKENT FILING DATE: 200-03-02 ; NUMBER OF SEQ ID NOS: 17 ; SOFTWARE: PatentIn Ver. 2.0 ; SEQ ID NO 7	
FILEREFERENCE: 1049-1-017 FURRENT APPLICATION NUMBER: US/09/517,605 FURRENT APPLICATION NUMBER: US/09/517,605	
APPLICANT: Geijtenbeck, Theo ; APPLICANT: Geijtenbeck, Theo ; TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO	
; APPLICANT: Kittman, Dan R. ; APPLICANT: Kwon, Douglas S. ; APPLICANT: van Koovk, Yvette	
SULT 6 -09-517-605-7 -09-517-605-7	. C 20
Db 681 GTGCTAGCTTTCCAGAAGGCCTCCAG 706	0
QY 601 GTGCTAGCTTTCCAGAAGGCCTCCGG 626	O
Db 621 ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG 680	D
OY 541 ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG 600	O
Db 561 AAAAACATACAGGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC 620	U
QY 481 AAAAACATACAGGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC 540	ø
Db 501 CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT 560	U
QY 421 CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT 480	Ø
Db 441 CTAGTGTTCGGATTGACTGCCAACTCTGACACCCACCTGCTTCAGGGGCAGAGCCCTGACC 500	b
QY 361 CTAGTGTTCGGATTGACTGCCAACTCTGACACCCCACCTGCTTCAGGGGCAGAGCCTGACC 420	O
Db 381 ATAGAAGACTCAGATACCTTACATCTGTGAAGTGGAGGACGAGGAGGTGCAATTG 440	۵
Qy 301 ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACGAGGAGGAGGTGGAATTG 360	O
Db 321 GACTCAAGAAGCCTTTGGGACCAAGGAAACTTCCCCCTGATCATCAAGAATCTTAAG 380	0
QY 241 GACTCAAGAAGACCTTTGGGACCAAGGAAACTTCCCCCTGATCATCAAGAATCTTAAG 300	o
Db 261 ATTCTGGGAAATCAGGGCTCCTTCTTAACTAAAGGTCCAAGCTGAATGATCGCGCT 320	D

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RESULT 7
US-09-023-655-1013
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                         TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                             CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
ANAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-(
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
                                                                                                                                                                                                                                                                                                                                    ZIP: 94304

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/09/023,655
FILING DATE: HEREWITH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Cocks, Benjamin G. APPLICANT: Susan G. Stuart APPLICANT: Jeffrey J. Seilhamer TITLE OF INVENTION: COMPOSITION TITLE OF INVENTION: EXPRESSION NUMBER OF SEQUENCES: 1508
                                                                                                                                                                                                                                                             CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PH
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
 TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                        LENGTH:
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: CALIFORNIA
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                                                         1742 base pairs
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                                                                                                                                                                                                                        Sequence 1, Application PC/TUS9208090
GENERAL INFORMATION:
APPLICANT: Tang, J. N.
TITLE OF INVENTION: Fusion Protein Genes
TITLE OF INVENTION: Aids
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS

CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick & Cody
STREET: 100 Peachtree Street

STREET: 100 Pe CITY: Atlanta STATE: Georgia COUNTRY:

30303 Georgia NUMBER OF SEQUENCES:

Application

PC/TUS9208090

for Treatment

of.

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; IMMEDIATE SOURCE:
; LIBRARY: GENBANK
; CLONE: g179143
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Best Local Similarity
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            GTGCTAGCTTTCCAGAAGGCCTCCGG
                                                                    ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAAATAGACATCGTG
                                                                                                                                                                              CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT
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                                                                                                                       AAAACATACAGGGGGGAAGACCCTCTCCGGTGTCTCAGCTGGAGCTCCAGGATAGTGGC
                                                                                                                                                                CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT
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GTGCTAGCTTTCCAGAAGGCCTCCAG
                                                    ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
                                                                                                       AAAAACATACAGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC
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Pred. No. 5.7e-138;
0; Mismatches 1;
                         626
701
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Best Local Sim
Matches 625;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 404-572-6555
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2465 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: NUCLEIC ACID
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (ge
HYPOTHETICAL: NO
ANTI-SENSE: NO
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            REFERENCE/DOCKET NUMBER: OM TELECOMMUNICATION INFORMATION: TELEPHONE: 404-572-6508
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.
REGISTRATION NUMBER: 31,284
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08090
FILING DATE: 19920922
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 2460..2465
OTHER INFORMATION: /note= "Restriction site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 1..6
OTHER INFORMATION: /note= "Restriction site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ORGANISM: Ho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
                                                                                                                                                                                                      381
                                                                                                                                                                                                                        301 ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGAGGTGCAATTG
                                                                                                                                                                                                                                                                      321
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                       AAAAACATACAGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC
                                                                                                   CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCCTCAGTGCAATGTAGGAGTCCAAGGGGGT
                                                                                                                                                                    CTAGTGTTCGGATTGACTGCCAACTCTGACACCCCACCTGCTTCAGGGGCAGAGCCTGACC
                                                                                                                                                                                                                                                                       GACTCAAGAAGCCTTTGGGACCAAGGAAACTTCCCCCTGATCATCAAGAATCTTAAG
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                                                                   CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT
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E: Epithelial
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Pred. No. 6.3e-138;
0; Mismatches 1;
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Patent No. 5
                                                                                                                                                   Matches
                                                                                                                                                                 Query Match
Best Local S
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FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,56;
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,96;
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEPAX: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION:
APPLICANT: Seed,
APPLICANT: Banapo
                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1304 base pairs
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APPLICATION 10MBER: US/08/284,5
FILING DATE: 02-AUG-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/195,395
                                                                                                                                                                                                                                           STRANDEDNESS:
TOPOLOGY: lin
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02110

COMPUTER READABLE FORM:
MEDIOW TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
                                                                                                                                                                   Local Similarity
                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
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STATE: MA
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                                                                                                              1 ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA
                                   GCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAAAAAAAGGGGGATACAGTGGAACTGACC
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Romeo, Charles
                                                                                                                                                   Conservative
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                                                                                                                                                 43.2%; Score 622.8; DB 2; 99.7%; Pred. No. 1.3e-137; cive 0; Mismatches 2;
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                                                                                                                                                                                      Length 1304;
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RESULT 10
US-09-218-950-28
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                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 28,
                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM COmpatil
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for
                                                                                                             COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/218,950
           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/284,391
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
                                                                                                                                                                                                                                                                                                     APPLICANT: KOlanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING
                                                                                                                                                                                                                                                                                                                                                        APPLICANT:
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ADDRESSEE: Clark & Elbing LLP
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                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                    STREET: 176 F
CITY: Boston
STATE: MA
COUNTRY: USA
ZIP: 02110
                                                                                                    FILING DATE:
                                                                                      CLASSIFICATION:
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Romeo, Charles
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RESULT 11
US-08-394-388A-28
; Sequence 28, Application
; Patent No. 6753162
; GENERAL INFORMATION:
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-218-950-28
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Best Local Similarity
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APPLICATION NUMBER: 07/665,96
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 0078
TELECHMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEPHONE: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA
                             GTGCTAGCTTTCCAGAAGGCCTCCGG
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                                                                                                           ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
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Pred. No. 1.3e-137;
0; Mismatches 2;
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SEQUENCE CHARACTERISTICS:
LENGTH: 1304 base pairs
TYPE: nucleic acid
STRANDENNESS: single
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 43.2%; Score 622.8; DB 4; Length 1304; Best Local Similarity 99.7%; Pred. No. 1.3e-137; Matches 624; Conservative 0; Mismatches 2; Indels 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ for Windows Version 2.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/394,388A
FILING DATE: 24-FEB-1995
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/284,391
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 01-847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 00786/247001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STATE: MA
COUNTRY: USA
ZIP: USA
ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Seed, Brian
APPLICANT: Banapour, Babak
APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
NUMBER OF SEQUENCES: 53
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
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CITY: B
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231
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	MOLECULE TYPE: DNA (genomic)	
	STRANDEDNESS: double	
	TYPE: nucleic acid	·. ··
	TERISTICS:	
	200154	
	TELEFAX: (617) 542-8906	
	FORMATION:	
	REFERENCE/DOCKET NUMBER: 00786/119002	
	NAME: Clark, Paul T.	· ·
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	ът 7,	٠
	07/665 061	
	APPLICATION NUMBER: US/07/847,566	
	APPLICATION NUMBER: US/08/203,866	٠
	CLASSIFICATION: 435 PRIOR APPLICATION DATA:	
	CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/417.495	
	ordperfect (Version 5.0)	
	S/2 Model 50Z or 5	
	COMPUTER READABLE FORM: MEDIUM TYPE: 3.5" Diskette, 1.44 Mb	 .
	ZIP: 02110-2804	٠
	STATE: MA	
	STREET: 225 Franklin Street CITY: Boston	٠
	ADDRESSEE: Fish & Richardson	·. ·.
	NUMBER OF SEQUENCES: 27	
Chimeras	TITLE OF INVENTION: Redirection of Cellular Immunity by	
	Brian et al	
	equence 2, Applicat atent No. 5843728	٠. ٠.
	SULT 12 -08-417-495-2	RE US
	711 GIGCTAGCTTTCCAGAAGGCCTCCAG 736	밁
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TAGACATCGTG 710	651 ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG	문
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AGAGCCTGACC 530	471 CTAGTGTTCGGATTGACTGCCAACTCTGACACCCACCTGCTTCAGGGGCAGAGCCCTGAC	밁
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RESULT 13
US-08-284-391B-2
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                                                                                                                                                                                                                                                                    Sequence 2, Application Patent No. 5851828 GENERAL INFORMATION:
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Best Local Similarity
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                                                                                     APPLICANT: Seed, Brian
APPLICANT: Banapour, Babak
APPLICANT: Romeo, Charles
APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
CORRESPE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
                                            STATE: MA
COUNTRY: USA
ZIP: 02110
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IBM Compatible
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99.7%;
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Pred. No. 1.3e
0; Mismatches
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1.3e-137;
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; STRANDEDNESS: double
; TOPOLOGY: linear
; MOLECULE TYPE: CDNA
US-08-284-391B-2
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SOFTWARE: FASESEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/284,391B
FILING DATE: 02-AUG-1994
CCLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,338
APERICATION NUMBER: 35,338
REGISTRATION NUMBER: 35,338
REGISTRATION NUMBER: 35,338
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPAX: 617-428-7045
TELEX:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1389 base pair
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
                             541
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                                                                                                                                                                                                                                                                       ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGTGCAATTG
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                ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
                                                              AAAAACATACAGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC
                                                                               AAAAACATACAGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC
                                                                                                                                            CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT
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   ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
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Pred. No. 1.3e-137;
0; Mismatches 2;
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RESULT 14
US-09-218-950-2
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US-09-218-950-2
                                                                                                                                                                           Query Match
Best Local Similarity 99.7
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Patent No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/284,391
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/ACENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 GENERAL INFORMATION:
APPLICANT: Seed, 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: Fast-SEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compati
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Banapour, Babak
APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED
TITLE OF INVENTION: CELLS BY
                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                     TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEFAX: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/09/218,950
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                                                                                                                                                                                                                                                                                                                                                              LENGTH:
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TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCAACCAGATAAAG
                                                                                                                  ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA
                                                                                                                                      ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA
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                                       GCAGCCACTCAGGGAAACAAAGTGGTGCTGGGCAAAAAAAGGGGGATACAGTGGAACTGACC
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Pred. No. 1.3e-137;
0; Mismatches 2;
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US-08-394-388A-2
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                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM Compatible
OPERATING SYSTEM: DO SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/394,388A
FILING DATE: 24-FEB-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US/08/284,391
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 08/195,395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Seed,
APPLICANT: Banapo
                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                STREET: 176 I
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
                                                                                                                                                                                                                                                                                                                                             COUNTRY: USA
ZIP: 02110
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Banapour, Babak
Romeo, Charles
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SEQUENCE CHARACTERISTICS:
LENGTH: 1389 base pairs
TYPE: nucleic acid
STRANDENNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 43.2%;
Best Local Similarity 99.7%;
Matches 624; Conservative
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NAME: Elbing, Karen L
REGISTRATION UNDEER: 35,238
REFERENCE/DOCKET NUMBER: 0078
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEPAX: 617-428-7045
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                 GTGCTAGCTTTCCAGAAGGCCTCCGG 626
                                                                        ACCTGGACATGCACTGTCTTGCAGAACCAGAAGGAGGTGGAGTTCAAAATAGACATCGTG 600
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GTGCTAGCTTTCCAGAAGGCCTCCAG 626
                                                       ACCTGGACATGCACTGTCTTGCAGAACCAGAAGGAAGGTGGAGTTCAAAATAGACATCGTG
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Pred. No. 1.3e-137;
O; Mismatches 2;
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Search completed: September Job time: 300 secs

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2005, 10:22:34

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scoring table:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Run on:
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1440
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                                                                                                                                                   /cgn2_6/ptodata/1/pubpna/US09A PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US09B PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/US09 NEW PUB.seq:*
/cgn2_6/ptodata/1/pubpna/US10A FUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/US10C PUBCOMB.seq:*
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/cgn2_6/ptodata/1/pubpna/USO6_PUBCOMB.seq:*
/cgn2_6/ptodata/1/pubpna/USO7_NEW_PUB.seq:*
/cgn2_6/ptodata/1/pubpna/PCTUS_PUBCOMB.seq:*
                _6/ptodata/1/pubpna/US10H_PUBCOMB.seq:*
6/ptodata/1/pubpna/US10I PUBCOMB.seq:*
_6/ptodata/1/pubpna/US10_REW PUB.seq:*
6/ptodata/1/pubpna/US11A_RUBCOMB.seq:*
_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
_6/ptodata/1/pubpna/US11_NEW_PUB.seq:*
_6/ptodata/1/pubpna/US10_NEW_PUB.seq:*
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6/ptodata/1/pubpna/US08_PUBCOMB.seq:*
_6/ptodata/1/pubpna/US60_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

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Result No.	O	Query Match Length DB	Length	DB	ID	Description
ы	625			18	US-10-612-192-3	Sequence 3, Appli
2	624.4	43.4	1377	14	US-10-103-597A-38	Sequence 38, Appl
ω	624.4	43.4	1377	15	US-10-188-444-38	Sequence 38, Appl
4	624.4	43.4	1742	14	US-10-151-274-7	Sequence 7, Appli
ហ	624.4	43.4	1742		US-10-641-643-1013	Sequence 1013, Ap
Q	622.8	43.2	1304		US-09-939-537-28	Sequence 28, Appl
7	622.8	43.2	1389	10	US-09-939-537-2	Sequence 2, Appli

ALIGNMENTS

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US-10-612-192-3
; Sequence 3, Application US/10612192
; Publication No. US20040076636A1
; GENERAL INFORMATION:
   APPLICANT: Pal, Ranajit
   APPLICANT: Waitham, Phillip
   APPLICANT: Whitney, Stephen
   APPLICANT: Keen, Timothy
   APPLICANT: Kalyanaraman, V.S.
   TITLE OF INVENTION: HIV Immunogenic Complexes
   FILE REFERENCE: 00711 CIP
   CURRENT FILING DATE: 2003-07-02
   PRIOR APPLICATION NUMBER: US/10/612,192
   CURRENT FILING DATE: 2001-07-17
   PRIOR APPLICATION NUMBER: US 09/905,962
   PRIOR APPLICATION NUMBER: US 09/479,675
   PRIOR APPLICATION NUMBER: US 09/075,544
   PRIOR FILING DATE: 1998-05-11
   NUMBER OF SEQ ID NOS: 3
   SOPTWARE: PATORIES DIA
   ORGANISM: Artificial
   FEATURE: DNA
   ORGANISM: Artificial
   FEATURE: OTHER INFORMATION: Expression Vector PTK13+Neo4
   US-10-612-192-3
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Gaps

120

60

180

180

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SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 38

LENGTH: 1377

TYPE: DNA

ORGANISM: Homo sapiens
FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1377)

US-10-103-597A-38
                                                                                                                                                  Sequence 38, Application US/10103597A
Publication No. US20030096432A1
GENERAL INFORMATION:
APPLICANT: Jakobsen, Bent Karsten
TITLE OF INVENTION: Screening Methods
FILE REFERENCE: 102286.142
CURRENT APPLICATION NUMBER: US/10/103,597A
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: PCT/GB00/03579
PRIOR APPLICATION NUMBER: PCT/GB00/03579
PRIOR FILING DATE: 2000-09-18
PRIOR FILING DATE: 1999-09-21
PRIOR FILING DATE: 1999-09-21
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US-10-103-597A-38
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Best Local Similarity
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                                                                                             Sequence 38, Application US/10188444

Publication No. US20030104635A1

GENERAL INFORMATION:
APPLICANT: Jakobsen, Bent Karsten
TITLE OF INVENTION: Screening Methods
FILE REFERENCE: 102286.142 (CIP)
CURRENT APPLICATION NUMBER: US/10/188,444

CURRENT FILING DATE: 2002-07-02
PRIOR APPLICATION NUMBER: PCT/GB00/03579
PRIOR APPLICATION NUMBER: GB 9922352.1
PRIOR APPLICATION NUMBER: GB 9922352.1
PRIOR FILING DATE: 1999-09-21
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0

SEQ ID NO 38
LENGTH: 1377
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Best Local Similarity
Matches 625; Conserv
   FEATURE:
NAME/KEY: CDS
LOCATION: (1)...(1377)
                                                   TYPE: DNA
ORGANISM: Homo sapiens
                                                                                    LENGTH: 1377
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Pred. No. 6.6e-171;
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APPLICANT: Littman, Dan R.
APPLICANT: Kwon, Douglas S.
APPLICANT: Won Kooyk, Yvette
APPLICANT: Geljtenbeck, Tneo
TITLE OF INVENTION: METHODS OF USING A FACIL
TITLE OF INVENTION: INTO
TITLE OF INVENTION: CELLS
FILE REFERENCE: 1049-1-017
CURRENT APPLICATION NUMBER: US/10/151,274
CURRENT FILING DATE: 2002-05-20
PRIOR APPLICATION NUMBER: US/9/517,605
PRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
LENGTH: 1742
TYPE: DNA
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US-10-151-274-7
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Best Local S
Matches 625
                                                                                                                                                                                                                                                               Sequence 7, Application US/10151274 Publication No. US20030064071A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Local Similarity
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99.8%;
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Pred. No. 6.6e-171;
0; Mismatches 1;
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US-10-151-274-7
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Best Local Simi
Matches 625;
                                                                                                                                                                                                                                Sequence 1013, Application US/10641643
Publication No. US20040077003A1
GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
   CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                        Susan G. Stuart
Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE
NUMBER OF SEQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS,
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Pred. No. 7.1e-171;
0; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                        626
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; SEQUENCE DESCRIPTION: SEQ ID NO: 1013 US-10-641-643-1013
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Best Local Similarity
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APPLICATION NUMBER: «Unknown»

FILING DATE: «Unknown»

ATTORNEY/AGENT INFORMATION:

NAME: Zeller, Karen J.

REGISTRATION NUMBER: 37,071

REFERENCE/DOCKET NUMBER: PA-0001 US

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 1742 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
IMMEDIATE SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/641,643
FILING DATE: 14-Aug-2003
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GTGCTAGCTTTCCAGAAGGCCTCCGG 626
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                                            ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
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llarity 99.8%;
Conservative
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Pred. No. 7.1e-171;
0; Mismatches 1;
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LENGTH: 1304 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: CDNA
SEQUENCE DESCRIPTION: SEQ ID NO: 28:
US-09-939-537-28
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US-09-939-537-28
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Best Local Similarity
Matches 624; Conserv
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APPLICANT: Seed
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:

APPLICATION NUMBER: 08/284,391
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
FILING DATE: 07-MAR-1991
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTMARE: FRAETSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
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ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
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                                                                                                                                                                                                                                                    676 GTGCTAGCTTTCCAGAAGGCCTCCAG
                                        121
                                                                                                                                                                                                                                                                                                                                                                                                tch 43.2%; al Similarity 99.7%; 624; Conservative
                                                                                                                                                                                     61
                                                                                                                                                                  TGTACAGCTTCCCAGAAGAAGAAGAATACAATTCCACTGGAAAAACTCCAACCAGATAAAG
                                                                                                               GCAGCCACTCAGGGAAACAAAGTGGTGCTGGGCAAAAAAAGGGGGATACAGTGGAACTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/09/939,537 FILING DATE: 24-Aug-2001 CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANI: Succession of the control of th
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                                                                                                                                                                                                                                                                                                                                                                                                    Score 622.8; DB 10;
Pred. No. 1.9e-170;
0; Mismatches 2;
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RESULT 7
US-09-939-537-2
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APPLICATION NUMBER: 08/284,391
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                   COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,537
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                         COUNTRY: USA
ZIP: 02110
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEB: Clark & Elbing LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
CELLS BY CHIMERIC CD4 RECEPTOR- BE
                                                                                                                                                        PRIOR APPLICATION DATA:
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                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                               STATE: MA
                                                                                                                                                                                                                                                                                                                                                                           CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                                STREET: 176 Federal Street
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Romeo, Charles
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MOLECULE TYPE: CDNA

SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-939-537-2
                                                                                     RESULT 8
US-09-243-008-2
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 Sequence 2, Application US/09243008
Publication No. US20040005334A1
GENERAL INFORMATION:
APPLICANT: Seed, Brian et al.
APPLICANT: Seed, Brian et al.
TITLE OF INVENTION: Redirection of Cellular Immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches 624; Conservative
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Best Local (
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SEQUENCE CHARACTERISTICS:
LENGTH: 1389 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00'
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                             GTGCTAGCTTTCCAGAAGGCCTCCGG 626
                                                                                                                                                                                                                                             ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
                                                                                                                                                                                                                                                                                                               AAAAACATACAGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC
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                                                                                                                                                                                                                                                                                             AAAAACATACAGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC
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TELEFAX: 617-428-7045
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Pred. No. 1.9e-170;
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US-09-243-008-2
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Best Local Similarity 99.7%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEX: 200154

INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1389 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/08/394,176
FILING DATE: SEPTEMBER 11,1995
APPLICATION NUMBER: 08/203,866
FILING DATE: February 28, 1994
APPLICATION NUMBER: 07/847,566
FILING DATE: March 6, 1992
APPLICATION NUMBER: 07/665,961
FILING DATE: March 7, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Karen F. Lech, Ph.D
REGISTRATION NUMBER: 35,238
REGISTRATION NUMBER: 35,238
REGISTRATION NUMBER: 00786/270001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: Wordperfect (Version 5.0)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/243,008 FILING DATE: 02-Feb-1999 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
CORDENCE: Fish & Richardson
STREET: 225 Franklin Street
361
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CTAGTGTTCGGATTGACTGCCAACTCTGACACCCACCTGCTTCAGGGGCAGAGCCTGACC
                                                            ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGAGGTGCAATTG
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                                       ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGTGCAATTG
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Pred. No. 1.9e-170;
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Sequence 3, Application US/09939537
Publication No. US20030138410A1
GENERAL INFORMATION:
                                                                                                                                               TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FBASELSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,537
FILING DATE: 24-Aug-2001
CLASSIFICATION: cUnknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                           REFERENCE/DOCKET NUMBER: TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
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MEDIUM TYPE: Diskette
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ADDRESSEE: Clark & Elbing LLP
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
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                                                                                                                                                                                                                                                                                                                                                                                                APPLICATION NUMBER: 08/284,391
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
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                                                                         LENGTH: 1599 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                       TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CITY: Boston
STATE: MA
                                                                                                                                                                                                                           TELEFAX: 617-428-7045
                                                                                                                                                                                                                                                   TELEPHONE: 617-428-0200
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OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
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Romeo, Charles
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RESULT 10
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                                                                                                                                                                                                                             Sequence 3, Application US/09243008
Publication No. US20040005334A1
GENERAL INFORMATION:
APPLICANT: Seed, Brian et al.
TITLE OF INVENTION: Redirection of Cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local
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STATE: MA
COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55XX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.)
SOFTWARE: Wordperfect (Version 5.0)
CURRENT APPLICATION DATA:
                                                                                                                                                          NUMBER OF SEASON.
CORRESPONDENCE ADDRESS:
Fish & Richardson
ADDRESSEE: Fish & Richardson
225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                601
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                                                                                                                                                CITY: Boston
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Pred. No. 2e-170;
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Best Local S
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1599 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICATION NUMBER: US/09/243,008
FILLING DATE: 02-Feb-1999
PRIOR APPLICATION DATE: US/08/394,176
APPLICATION NUMBER: US/08/394,176
FILLING DATE: SEPTEMBER 11,1995
APPLICATION NUMBER: 08/203,866
FILLING DATE: February 28, 1994
APPLICATION NUMBER: 07/847,566
FILLING DATE: March 6, 1992
APPLICATION NUMBER: 07/665,961
FILLING DATE: March 7, 1991
AFTORNEY/AGENT INFORMATION: NAME: KATEGN F. LECh, Ph.D
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/270001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO:
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                                                                                                  AAAAACATACAGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC
                                                                                                                                                                             CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT
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                                          ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
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                      ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
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Pred. No. 2e-170;
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TOPOLOGY: linear
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MOLECULE TYPE: cDNA
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SEQUENCE DESCRIPTION: SEQ ID NO: 1:
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Publication No. US20030138410A1
GENERAL INFORMATION:
                                                                                                                                                                                            Matches
                                                                                                                                                                                                          Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                     TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: 08/284,391
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/65,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Elbing, Karen L
REGLSTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/247001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: PastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,537
FILING DATE: 24-Aug-2001
CLASSIFICATION: <UNknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Seed, Brian
APPLICANT: Seed, Brian
Banapour, Babak
Romeo, Charles
Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
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MEDIUM TYPE: Diskette
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ADDRESSEE: Clark & Elbing LLP
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                                                                                                                 ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTTGGTGCTACTGGCGCTCCTCCCA
                                                                                                                                                                                                                                                                                                                                         LENGTH: 1728 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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                                                                                                                                                                                        Score 622.8; DB 10;
Pred. No. 2.1e-170;
0; Mismatches 2;
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US-09-243-008-1
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Sequence 1, Application US/09243008
Publication No. US20040005334A1
GENERAL INFORMATION:
APPLICANT: Seed, Brian et al.
APPLICANT: Seed, Brian et al.
Receptor Chimeras
                                                 COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM P.C. DOS (Version 3.3
OPERATING SYSTEM: IBM P.C. DOS (Version 3.3
SOFTWARE: Worddperfect (Version 5.0)
CURRENT APPLICATION NOMBER: US/09/243,008
FILING DATE: 02-Feb-199
PRIOR APPLICATION NUMBER: US/08/394,176
FILING DATE: SEPTEMBER 11,1995
APPLICATION NUMBER: 08/203,866
FILING DATE: FEBTUARY 28, 1994
APPLICATION NUMBER: 07/847,566
FILING DATE: March 6, 1992
APPLICATION NUMBER: 07/665,961
FILING DATE: March 7, 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
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COUNTRY: USA
ZIP: 02110-2804
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; TOPOLOGY: linear; MOLECULE TYPE: DNA (genomic); SEQUENCE DESCRIPTION: SEQ ID NO: US-09-243-008-1
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                                                                                                                  RESULT 13
US-09-891-119A-8
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Sequence 8, Application US/09891119A
Publication No. US20040013683A1
GENERAL INFORMATION:
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: DERIVATIVES OF SOLUBLE
FILE REFERENCE: 24577-CY-B
CURRENT APPLICATION NUMBER: US/09/891,119A
CURRENT FILING DATE: 2001-06-25
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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TELEPHONE: (617) 542-5070
TELEPAX: (617) 542-8906
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                     ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
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Pred. No. 2.1e-170;
0; Mismatches 2;
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; NUMBER OF SEQ ID NOS: 22
; SOFTWARE: PatentIn version 3
; SEQ ID NO 8
; LENGTH: 1742
; LENGTH: 1742
; TYPE: DNA
; ORGANISM: Human
US-09-891-119A-8
Sequence 1, Application US/10024329
Publication No. US20030157063A1

GENERAL INFORMATION:
APPLICANT: SANHADJI, Kamel
APPLICANT: TOURAINE, Jean-Louis
APPLICANT: LEROY, Pierre
APPLICANT: MEHTALI, Majid
TITLE OF INVENTION: Gene therapy using anti-
FILE REFERENCE: 10993
CURRENT APPLICATION NUMBER: US/10/024,329
CURRENT FILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO 1
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 622.8; DB 11,
Pred. No. 2.1e-170;
"" matches 2;
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anti-gp41 antibody

and cd4 immunoadhesin

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Sequence 169, Application US/10207655

Publication No. US20030118592A1

GENERAL INFORMATION:
APPLICANT: Ledbetter, Jeffrey A.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BIDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069 401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SEQ ID NO 169
LENGTH: 3084
TYPE: DNA
ORGANISM: Homo sapiens
US-10-207-655-169
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                                                                                                                                                                                                                             RESULT 15
US-10-207-655-169
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TYPE: DNA
ORGANISM: human
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Search completed: September 20, 2005, 16:05:03 Job time: 2461 secs

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Result
No.
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Maximum
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Maximum Match 100%
Listing first 45 s
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Perfect score:
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         Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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BG685053	AW406380	AW407282	BP344191	CB997693	BP344125	BP367248	CK835626	AL553628	AW752358	BP277052	CO246525	CB052685	AU136822	BP300162	BP345874	BP287803	BP339950	BP361417	AW752367	CO248544
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ALIGNMENTS

Qy	Qy Db	dg VQ	gb Qy	Query Ma Best Loo Matches	ORIGIN	FEATURES	AUTHORS TITLE JOURNAL COMMENT	SOURCE SOURCE ORGANISM	RESULT 1 CD609192/c LOCUS DEFINITION ACCESSION VERSION
181 ATTCTGGGAAATCAGGGCTCCTTCTTAACTAAAGGTCCATCCA	121 TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCAACCAGATAAAG 180	61 GCAGCCACTCAGGGAAAGAAGTGGTGGTGGGCAAAAAAGGGGATACAGTGGAACTGACC 120	1 ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA 60	<pre>/ Match 43.2%; Score 622.8; DB 6; Length 783; Local Similarity 99.7%; Pred. No. 2.5e-152; les 624; Conservative 0; Mismatches 2; Indels 0; Gaps 0;</pre>	/n/ /n/ /n/ /n/	Incyce venomics, Inc. 3160 Porter Dr., Palo Alto, CA 94304, USA Tel: 6508454102 Email: gfu@incyte.com. Location/Qualifiers	u,G.K., Wang,J.7 ircular rapid an ircular rapid an xtension cloning enomics 84 (1), ontact: Fu GK	Homo sapiens (human) Homo sapiens Homo sapiens Homo sapiens Elikaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 783)	

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BX438745
5-PRIME,
BX438745
                                                                                                                                                                                                                                                 Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EWNY cedex - FRANCE
Email: segref@genoscope.cns.fr, Web : www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the DCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
                                                                                                                                                                                                                                                                                                                                                                                  Mammalia; Eutheria; Primates; Catarrhini; Homin
1 (bases 1 to 932)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 15, 2003 this sequence version replaced
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Homo
                                                                                                                                                                                   This sequence belongs to sequence cluster 6485.r For more information about this cluster, see http://www.genoscope.cns.fr/cdna?s=CSODE002AD01QP1&c=6485.Location/Qualifiers
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/clone_lib="Homo saplens PLACENTA"
/note="Vector: pcMVSPORT 6; lst strand cDNA was primed
/note="Vector: pcMVSPORT 6; lst strand cDNA was primed
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the Not I and EcoRV sites of the pcMVSPORT 6 vector.
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/clone="CSODE002YG01"
                                                                                                                                                    organism="Homo
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BI838409
BI838409.1 GI
                                                                                                Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalla; Eutheria; Primates; Catarrhini; Hominidae;
1 (Dases 1 to 816)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collect
   Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium
                                                                   Unpublished (1999)
Contact: Robert Strausberg,
                                                                                                                                                                                     Homo sapiens
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Plate: LLAM11559 row: b column:
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Clone distribution: MGC clone distribution information
                                      GGTGCTAGCTTTCCAGAAGGCCTCCGG 626
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Location/Qualifiers
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/note="Organ: pooled pancreas and spleen; Vector:
/note="Organ: pooled pancreas and spleen; Vector:
pcMV-SpORTG, Site 1: Not1; Site 2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
/clone="IMAGE:5222323"
/lab_host="DH10B"
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Pred. No. 5.2e-149;
n: Mismatches 3;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was grimed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
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5-PRIME,
BX457159
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This sequence belongs to sequence cluster 6485.r for more information about this cluster, see from y genoscope.cns.fr/cdna?s=CSOCAPOO6CH04QPl&c=6485.r.http://www.genoscope.cns.fr/cdna?s=CSOCAPOO6CH04QPl&c=6485.r.http://www.genoscope.cns.fr/cdna?s=CSOCAPOO6CH04QPl&c=6485.r.http://www.genoscope.cns.fr/cdna?s=CSOCAPOO6CH04QPl&c=6485.r.http://www.genoscope.cns.fr/cdna?s=CSOCAPOO6CH04QPl&c=6485.r.http://www.genoscope.cns.fr/cdna?s=CSOCAPOO6CH04QPl&c=6485.r.http://www.genoscope.cns.fr/cdna?s=CSOCAPOO6CH04QPl&c=6485.r.http://www.genoscope.cns.fr/cdna?s=CSOCAPOO6CH04QPl&c=6485.r.http://www.genoscope.cns.fr/cdna?s=CSOCAPOO6CH04QPl&c=6485.r.http://www.genoscope.cns.fr/cdna?s=CSOCAPOO6CH04QPl&c=6485.r.http://www.genoscope.cns.fr/cdna?s=CSOCAPOO6CH04QPl&c=6485.r.http://www.genoscope.cns.fr/cdna?s=CSOCAPOO6CH04QPl&c=6485.r.http://www.genoscope.cns.fr/cdna?s=CSOCAPOO6CH04QPl&c=6485.r.http://www.genoscope.cns.fr/cdna?s=CSOCAPOO6CH04QPl&c=6485.r.http://www.genoscope.cns.fr/cdna?s=CSOCAPOO6CH04QPl&c=6485.r.http://www.genoscope.cns.fr/cdna?s=CSOCAPOO6CH04QPl&c=6485.r.http://www.genoscope.cns.fr/cdna?s=CSOCAPOO6CH04QPl&c=6485.r.http://www.genoscope.cns.fr/cdna?s=CSOCAPOO6CH04QPl&c=6485.r.http://www.genoscope.cns.fr/cdna?s=CSOCAPOO6CH04QPl&c=6485.r.http://www.genoscope.cns.fr/cdna?s=CSOCAPOO6CH04QPl&c=6485.r.http://www.genoscope.cns.fr/cdna?s=CSOCAPOO6CH04QPl&c=6485.r.http://www.genoscope.cns.fr/cdna?s=CSOCAPOO6CH04QPl&c=6485.r.http://www.genoscope.cns.fr/cdna?s=CSOCAPOO6CH04QPl&c=6485.r.http://www.genoscope.cns.fr/cdna?s=CSOCAPOO6CH04QPl&c=6485.r.http://www.genoscope.cns.fr/cdna?s=CSOCAPOO6CH04QPl&c=6485.r.http://www.genoscope.cns.fr/cdna?s=CSOCAPOO6CH04QPl&c=6485.r.http://www.genoscope.cns.fr/cdna?s=CSOCAPOO6CH04QPl&c=6485.r.http://www.genoscope.cns.fr/cdna?s=CSOCAPOO6CH04QPl&c=6485.r.http://www.genoscope.cns.fr/cdna?s=CSOCAPOO6CH04QPl&c=6485.r.http://www.genoscope.cns.fr/cdna?s=CSOCAPOO6CH04QPl&c=6485.r.http://www.genoscope.cns.fr/cdna?s=CSOCAPOO6CH04QPl&c=6485.r.http://www.genoscope.cns.fr/cdna?s=CSOCAPOO6CH04QPl&c=6485.r.http
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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                                                                                                                                                                                                                                                             CTGTACAGCTTCCCAGAAGAAGAGAGACATACAATTCCACTGGAAAAACTCCCAACCAGATAAA 179
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                                                  GATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGTGCAATT
                                                                                                                                                                                                                                                                                                                                              CTGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCAACCAGATAAA
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  GATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGTGCAATT
                                                                                                                                                                                                                               Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="THYMUS"
/clone_Tib="Homo sapiens THYMUS"
/clone_Tib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library was not normalized."
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/clone="CS0CAP006YP07"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Homo sapiens"
/mol_type="mRNA"
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Pred. No. 3.6e-146;
1; Mismatches 2;
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Robert Strausberg, Ph.D.

Email: cgapbs-r@mail.nih.gov

Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 801)

NIH-MGC http://mgc.nci.nih.gov/.

National Institutes of Health, Mammalian Gene Collection (MGC)

Unpublished (1999)
        1 ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA
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B1822118
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603039813F1 NIH_MGC_115 Homo
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High quality sequence stop: 793.
Location/Qualifiers
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                                                               Conservative
                                                                                                                                                                      /mol_type="manual"
/mol_type="manual"
/db_xref="taxon:9606"
/dlone="IMAGE:5180642"
/lab_host="MAGE:5180642"
/lab_host="MIH MGC 115"
/clone_lib="NIH MGC 115"
/clone_lib="NIH MGC 115"
/clone_sports; site_1: NotI; Site_2: EcoRV (destroyed); RNA source anonymous pool of 6 male brains, age range 23-27; l male lung, age 27; and 1 male testis, age 69. Library is oligo-dT primed and directionally cloned (EcoRV site is destroyed upon cloning). Average insert size 1.8 kb, insert size range 1-3 kb. Library is normalized and enriched for full-length clones and was constructed by C. Gruber (Invitrogen). Research Genetics tracking code 021. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   organism="Homo sapiens"
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99.4%;
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                                                         Score 598.8; DB 4;
Pred. No. 5.1e-146;
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sapiens cDNA clone IMAGE:5180642 5',
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                                                                                                                                                                   Contact: Robert Strausberg, Ph.D.
Email: cgapbs-@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
                                                                                                                                                                                                                                                                                                                                                             Homo sapiens
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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High quality sequence stop: 832.
Location/Qualifiers
                                                                                   found through the I.M.A.G.E. Consortium/LLNL http://image.llnl.gov Plate: LLAM11569 row: m column: 20
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/clone lib="NIH MGC 120"
/note-Torgan: pooled pancreas and spleen; Vector:
/note-Torgan: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site 1: NotI; Site 2: ECGRV (destroyed); RNA
source annonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."
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/lab_host="DH108"
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Tissue procurement: Life Technologies, Inc.
CDNA Library Preparation: Life Technologies, Inc.
CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MCC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAMN11454 row: n column: 03
High quality sequence stop: 782.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 176 ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collections (1999)
Contact: Robert Strausberg, Ph.D.
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                             GCTAGTGTTCGGATTGACTGCCAACTCTGACACCCCACCTGCTTCAGGGGCAGAGCCTGAC 419
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                                                                                                                                                GATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGTGCAATT 359
                                                                                                                                                                                                                                                                                                              TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCAACCAGATAACA
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/db_xref="taxon:9606"
/clone="IMAGE:5182274"
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/mol_type="mRNA"
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1 (bases 1 to 557)

Rual, J.F., Hirozane-Kishikawa, T., Hao, T., Bertin, N., Li, S., Dricot, A., Li, N., Rosenberg, J., Lamesch, P., Vidalain, P.O., Clingingsmith, T.R., Hartley, J.L., Esposito, D., Cheo, D., Moore, T., Simmons, B., Sequerra, R., Bosak, S., Doucette-Stamm, L., Le Peuch, C., Vandenhaute, J., Cusick, M.E., Albala, J.S., Hill, D.E. and Vidal, M. Human ORFeome Version 1.1: a Platform for Reverse Proteomics
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8403 Ful
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BACKWARD: CAAATGGGGCTACATGTCTTCGAAA
Insert Length: 557 Std Error: 21.00
Plate: 11064 row: 03 column: B
Seq primer: ACTGGCCGTCGTTTTACAACGTCGTGACTGGGAAAAC
High quality sequence start: 98
High quality sequence stop: 556
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Dana Farber Cancer Institute
1 Jimmy Fund Way Smith 858, F
Tel: 617 632 5180
Fax: 617 632 5739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             template DNA and ORF specific primers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Email: Marc Vidal@dfci.harvard.edu
ORF Sequence Tag (OST) of Gateway Entry construct. Each cloned
results from a PCR_reaction_using an MGC full-length cDNA as
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Res. (2004) In press
Contact: Vidal M
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Full Length cDNA from the Mammalian Gene Collection Homo
ens cDNA 5' similar to BC025782, mRNA sequence.
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               /note="Vector: mixed; The ORF8 were PCR amplified from the MGC (Mammalian Gene Collection) as of April 2004 and cloned by recombinational Gateway cloning into pDouR223 Donor vector. Reference : MGC (Mammalian Gene Collection) Program Team, Generation and Initial Analysis of more than 15,000 Full-Length Human and Mouse cDNA Sequences. PNAS, 2002, 99(26), 16899-16903"
                                                                                                                                                                      /mol_type="mRNA"
/db_xref="taxon:9606"
/tissue_type="mixed"
/clone_Tib="Full Length cDNA from the Mammalian Gene
Collection"
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 713)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D. Full-length cDNA libraries and normalization Unpublished (2001)

On May 15, 2003 this sequence version replaced gi:30771588.

Contact: Genoscope

Contact: Genoscope
                                                                                                               Homo sapiens (human)
                                                                                                                                                                    BX437619 Homo sapiens THYMUS 5-PRIME, mRNA sequence.
BX437619
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Genoscope - Centre National de Sequencage
2 rue Gaston Cremieux, CP 5706 - 91057 EVRY cedex - FRANCE
Email: segref@genoscope.cns.fr Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

This

sequence belongs to sequence cluster more information about this cluster, s

6485.r

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Homo sapiens
Eukaryota; Metazoa;
Mammalia; Eutheria;
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Location/Qualifiers
                                                                                                 mRNA sequence.
BI915265
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                                                                                   BI915265.1
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/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime end enriched, double-strand cDNA was digested with Not I and cloned the Not I and EcoRV sites of the pCMVSPORT 6 vector.
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/db_xref="taxon:9606"
/clone="CSOCAP007YD02"
/tissue_type="THYMUS"
                                                                                   GI:16179363
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 Chordata;
Primates;
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Pred. No. 2.6e-130;
1; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11626 row: j column: 03
High quality sequence stop: 717.
Location/Qualifiers
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National Institutes of Health, Mammalian
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Similarity
GTAAAAACATACAGGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTG
                                                                     CCCTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCTCAGTGCAATGTAGGAGTCCAAGGG
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/note="Organ: bTain; Vector: pCMV-SPORT6; Site_1: NotI;
/note="Organ: bTain; Vector: pCMV-SPORT6; Site_1: NotI;
/site_2: EcoRV (destroyed); RNA source anonymous pool of 3
fetal brains, female age 20 weeks, female age 24 weeks,
and male age 26 weeks. Library is oligo-dT primed and
directionally cloned (EcoRV site is destroyed upon
cloning). Average insert size 1.7 kb, insert size range
0.7-3.5 kb. Library is normalized and enriched for
full-length clones and was constructed by C. Gruber
(Invitrogen). Research Genetics tracking code 017. Note:
this is a NIH_MGC Library."
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/mol_type="mRNA"
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Pred. No. 3.8e-125;
0; Mismatches 1;
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3160 Porter Dr., Palo Alto,
Tel: 6508454102
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 (bases 1 to 679) Fu.G.K., Wang, J., Au-Young, J. and Stuve, L.L. circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes Genomics 84 (1), 205-210 (2004) Contact: Fu GK
                                                                                                                                                                                                                                                                                                                                                                                                                        1 ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; I
Mammalia; Eutheria; Primates; Catarrhini; Hominidae;
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CD609191.1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: gfu@incyte.com
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              CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT
                                                                      CTAGTGTTCGGATTGACTGCCAACTCTGACACCCTGCTTCAGGGGCAGAGCCTGACC
                                                                                                                            ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGAGGTGCAATTG
                                                                                                                                                                   GACTCAAGAAGAAGCCTTTGGGACCAAGGAAACTTTCCCCCTGATCATCAAGAATCTTAAG
                                                                                                                                                                                     GACTCAAGAAGAAGCCTTTGGGACCAAGGAAACTTCCCCCCTGATCATCAAGAATCTTAAG
                                                                                                                                                                                                                         TGTACAGCTTCCCAGAAGAAGAAGCATACAATTCCACTGGAAAAACTCCAACCAGATAAAG
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                                                    CTAGTGTTCGGATTGACTGCCAACTCTGACACCCCACCTGCTTCAGGGGCAGAGCCTGACC
                                                                                                             ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGTGCAATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /mol_type="mRNA"
/db_xref="taxon:9606"
/clone lib="FLP"
/note="Vector: pDrive Cloning Vector"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            organism="Homo sapiens"
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Pred. No. 9.7e-122;
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AU141298
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AU141298
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1532-3 Yana, Kisarazu, Chiba
Tel: 81-438-52-3975
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Contact: Takao Isogai
Genomics Laboratory
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EST.
                                                                                                                                                                                                                                                                                                                                    h 35.0%;
Similarity 97.2%;
22; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HRI human cDNA project
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                                                                      GACTCAAGAAGAAGCCTTTGGGACCAAGGAAACTTCCCCCCTGATCATCAAGAATCTTAAG
              ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGTGCAATTG
                                                                                                                            TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCAACCAGATAAAG
                                                                                                                                                                                   TGTACAGCTTCCCAGAAGAAGAGAGCATACAATTCCACTGGAAAAAACTCCAACCAGATAAAG
                                                      GACTCAAGAAGAAGCCTTTGGGACCAAGGAAACTTTCCCCCTGATCATCAAGAATCTTAAG
                                                                                                             732
THYRO1 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="THYRO1"
/note="Vector: pME18SFL3"
                                                                                                                                                                                                                                                                                                                                                                                                                       /mol_type="mRNA"
/db xref="taxon:9606"
/clone="THYRO1000359"
/tlssue type="thyroid gland"
/clone_Tib="THYRO1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Homo sapiens"
/mol_type="mRNA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
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Pred. No. 4.2e-121;
0; Mismatches 13;
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Indels

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Gaps

120

315

255

60

360

555

300

495

435 240

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Email: genomics@hri.co.jp
HRI human cDNA project, 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
Helix Research Institute.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawa
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 732)
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lgano,S. and
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REFERENCE
AUTHORS
TITLE
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CO246446
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Contact: Daniela S. Gerhard, Ph.D. Office of Cancer Genomics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian
Unpublished (1999)
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1 (bases 1 to 754)
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                          ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA 60
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                                                         33.9%;
llarity 96.6%;
Conservative
                                                                                                                              /tissue_type="Chondrosarcoma Lung Metastasis cell lines"
/lab host="DH10B (T1 phage resistant)"
/clone_lib="NIH_MGC_212"
/clone_lib="NIH_MGC_212"
/note="Organ: Lung; Vector: pYX-Asc; Site 1: EcoR I;
/note="Organ: Lung; Vector: pYX-Asc; Site 1: EcoR I;
/site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
grimer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Not I and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is GATAAGGCCA. Tissue was provided by Mary Hendrix."
                                                                                                                                                                                                                                                                                                                                            /mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:30924065"
                                                                                                                                                                                                                                                                                                                                                                                        organism="Homo sapiens"
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                                                         Score 488.8; DB 7;
Pred. No. 4.2e-117;
0; Mismatches 17;
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Tel: 319 335 8250
Fax: 319 335 9565
Email: bento-soares@uiowa.edu
Tissue Procurement: Mary Hendrix
CDNA Library preparation: Dr. M. Bento Soares, University of Iowa
CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa
DNA Sequencing by: Dr. M. Bento Soares, University of Iowa
Clone Distribution: Distribution information can be found at
http://genome.uiowa.edu/distribution/humanfl.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   710 bp
UI-HF ELO-avo-e-23-0-UI.rl NIH b
IMAGE:30563734 5', mRNA sequence
CF125444
                                                                                                                                                                                                                                                                                                                                                                                                                                  Coordinated Laboratory University of Iowa 375 Newton Road , 4156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Genome Res. 6 (9), 791-806 (1996) 97044477
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Bonaldo, M.F., Lennon, G. and Soares, M.B.
Normalization and subtraction: two approaches to fac
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Soares, MB
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                                                                                                                                                                             primer: pYX-5
                     /organism="Homo sapiens"
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/db_xref="taxon:9606"
/clone="IMAGE:30563734"
                                                                                                                                                     Location/Qualifiers
tissue_type="Chondrosarcoma Lung Metastasis cell lines"/
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CB052686
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ORGANISM
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VERSION
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NISC g109e06.y1 NCI_CGAP_Lei2 Homo sapiens
5', mRNA sequence.
CH052686
CH052686 G1:27790973
             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 694)

NCI-CGAP http://www.ncbi.nlm.nih.gov/ncicgap.

National Cancer Institute, Cancer Genome Anatomy Project (CGAP),
Tumor Gene Index.
                                                                                                                                                       Homo
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/clone_lib="NIH_MGC_212"
/note="Organ: Lung; Vector: pYX-Asc; Site 1: EcoR I;
/note="Organ: Lung; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Not I and then cloned
directionally into pyX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is GATAAGGCCA. Tissue was provided by Mary Hendrix."
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Email: cgapbs-r@mail.nih.gov
cDNA Library Preparation:
cDNA Library Arrayed by: The I.M.A.G.E. Consortium/LLNL
cDNA Sequencing by: National Institutes of Health Intramural
Sequencing Center (NISC)
Clone distribution: NCI-CGAP clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plate: LLAM8058 row: I column: 11
Seq primer: M13RP1 reverse primer (ABI).
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Plate: LLAM8058 rov
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  TAAAAACATACAGGGGGGG 498
                                                          CCTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCTCAGTGCAATGTAGGAGTCCAAGGGG
                                                                                                 GCTAGTGTTCGGATTGACTGCCAACTCTGACACCCCACCTGCTTCAGGGGCAGAGCCTGAC
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/tissue_type="leiomyosarcoma"
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/db_xref="taxon:9606"
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mol_type="mRNA"
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0; Mismatches 2;
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Job time : 5149 secs

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GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.

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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	&	7	6	5	4	ω	N	1	Result No.
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ALIGNMENTS

RESULT 1 ABP45023 ID ABP4 XX ABP4 XX ABP4 XX ABP4 XX BLyg XX BLyg XX BLyg XX BLyg XX BLyg XX Enmm XX Enmm XX Enmm XX Enmm XX Home XX H Homo sapiens. Human BLyS binding scrv SEQ ID 1034. 19-AUG-2002 ABP45023; ABP45023 standard; (first protein; entry) 259 ₿

BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AIDS; common variable immunodeficiency; acquired immunodeficiency syndrome.

WO200202641-A1.

10-JAN-2002

15-JUN-2001; 2001WO-US019110

16-JUN-2000; 2000US-0212210P: 17-OCT-2000; 2000US-0240816P: 16-MAR-2001; 201US-0276248P: 21-MAR-2001; 2001US-0277379P: 25-MAY-2001; 2001US-0293499P:

(HUMA-) HUMAN GENOME SCI INC. (CAMB-) CAMBRIDGE ANTIBODY TECHNOLOGY.

WPI; 2002-114799/15.

MS.

Barash SC,

Choi GH,

Vaughan T,

Hilbert D;

Antibodies against B Lymphocyte Stimulating polypeptides, diagnosis and treatment of cancers and immune disorders. useful for the

Page 1635-1636; 3148pp; English.

This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory,

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to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to chromosome 13q34 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scFvs) derived, preferably, from the variable heavy CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The present invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression and activity such as cancer, immune, and autoimmune disorders and diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP47930-ABP47228 represent the antibodies and fragments of the antibodies described in the method of the antibodies and fragments of the antibodies described in the method of the antibodies and fragments of the antibodies described in the method of the antibodies described in the method of the antibodies and fragments of the antibodies described in the method of the antibodies and fragments of the antibodies described in the method of the antibodies described in the antibodies 
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAlDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency; systemic lupus erythematosus; rheumatoid arthritis; CVID; AlDS; common variable immunodeficiency; acquired immunodeficiency syndrome.
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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to

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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNP) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS.
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17-CCT-2000; 2000US-024081EP.
16-MAR-2001; 2001US-0276248P.
21-MAR-2001; 2001US-0277379P.
25-MAY-2001; 2001US-0293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  BLys; B lymphocyte stimulator; TWP superfamily; human; cytostatic; tumour necrosis factor; B cell proliferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficiency;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (ALDS)). ABP43990-ABP47228 represent the antibodies and fragments of the antibodies are discounted.
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17-CCT-2000; 2000US-0240816P.
16-MAR-2001; 2001US-0276248P.
21-MAR-2001; 2001US-0277379P.
25-MAY-2001; 2001US-0293499P.
                     cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines tinhibit the expression and activity of BLyS. The antibodies bind
                                                                                             This invention describes novel antibodies that immunospec B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a metumour necrosis factor (TMF) super family and induces B c proliferation and differentiation. The antibodies of the
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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease
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17-CCT-2000; 2000US-0240816P.
16-MAR-2001; 2001US-0276248P.
21-MAR-2001; 2001US-0277379P.
25-MAY-2001; 2001US-0293499P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BLys; B lymphocyte stimulator; TNF superfamily; human; cytostatic; tumour necrosis factor; B cell prollferation; B cell differentiation; immunosuppressive; immunostimulant; immunomodulatory; antirheumatic; antiAIDS; vaccine; cancer; immune; autoimmune disorder; immunodeficie
                                                                                                                                                                                                                                                                                                                                                                         Antibodies against B Lymphocyte Stimulating polypeptides, diagnosis and treatment of cancers and immune disorders.
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This invention describes novel antibodies that immunospecifically bind to B Lymphocyte Stimulator (BLyS) polypeptides. BLyS is a member of the tumour necrosis factor (TRP) super family and induces B cell proliferation and differentiation. Immunostimulant, immunomodulatory, antitheumatic and antiAIDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be
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17-OCT-2000; 2000US-0240816P.
16-MAR-2001; 2001US-0276248P.
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tumour necrosis factor (TNF) super family and induces B cell proliferation and differentiation. The antibodies of the invention have cytostatic, immunosuppressive, immunostimulant, immunomodulatory, antirheumatic and antiAlDS activity and can be used in vaccines to inhibit the expression and activity of BLyS. The antibodies bind to BLyS and so may be used to detect and quantitate the presence of BLyS in biological samples and may be used in this way to diagnose disease associated with aberrant expression of BLyS. They may also be administered to treat diseases associated with aberrant BLyS expression
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             16-JUN-2000; 2000US-0212210P.
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16-MAR-2001; 2001US-027624BP.
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This invention relates to novel antibodies that immunospecifically bind cto B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to CC chromosome 13q34 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell CC chain antibody molecules (gcFvs) derived, preferably, from the variable heavy CDR3 region that immunospecifically bind to a polypeptide, or CC fragment thereof, of either human, murine, rat or monkey BLyS. The CC present invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the CC aberrant expression or inappropriate function of BLyS or its receptor. As Such, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple sclerosis, inflammatory CC disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and CC lymphoma. Accordingly, they can be described as exhibiting various
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                diseases, e.g. systemic lupus erythematosus, rheumatoid arthritis, immunodeficiency (e.g. common variable immunodeficiency (CVID) and acquired immunodeficiency syndrome (AIDS)). ABP43990-ABB47228 represent the antibodies and fragments of the antibodies described in the method of the introduced control of the control of 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g.
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This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to chromosome 13q34 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scFvs) derived, preferably, from the variable heavy CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The present invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders such, these compositions are useful for identifying immune disorders and liculding myasthenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such lymphoma. Accordingly, they can be described as exhibiting various
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Novel antibody that immunospecifically binds to (BLys), useful for detecting and treating diseas
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Pred. No.
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ses or disorders e.g.
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RESULT 11
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This invention relates to novel antibodies that immunospecifically bind CC to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to CC chromosome 13q34 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single CC chain antibody molecules (scFvs) derived, preferably, from the variable heavy CDR3 region that immunospecifically bind to a polypeptide, or CC fragment thereof, of either human, murine, rat or monkey BLyS. The CC present invention refers to the use of such antibodies in various methods CC for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders consolitions are useful for identifying immune disorders classifications and multiple sclerosis, inflammatory consolitions and proliferative disorders including leukaemia, carcinoma and CC lymphoma. Accordingly, they can be described as exhibiting various
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 20
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel antibody that immunospecifically binds to (BLys), useful for detecting and treating diseau rheumatoid arthritis, asthma and leukemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Example 1; SEQ ID NO 1497; 394pp; English
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19-DEC-2001; 2001US-0340817P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lymphocyte stimulator; BLy iferation; differentiation;
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ilarity 100.0%;
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RESULT 12
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XX Ruben
XX 
                      This invention relates to novel antibodies that immunospecifically bind to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to chromosome 1394 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scFvs) derived, preferably, from the variable heavy CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The present invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As concluding myasthenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as ALDS and proliferative disorders in the compositions are useful for identifying immune disorders concluding myasthenia gravis and multiple sclerosis, inflammatory
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Novel antibody that immunospecifically binds to a B lymphocyte stimulator (BLys), useful for detecting and treating diseases or disorders e.g. rheumatoid arthritis, asthma and leukemia.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Example 1; SEQ ID NO 1247; 394pp; English
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Best Local :
                        to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to chromosome 13g34 and encodes a protein that is a member of the tumour necrosis factor superfamily and induces both in vivo and in vitro B cell proliferation and differentiation. Specifically, it refers to single chain antibody molecules (scFvs) derived, preferably, from the variable heavy CDR3 region that immunospecifically bind to a polypeptide, or fragment thereof, of either human, murine, rat or monkey BLyS. The present invention refers to the use of such antibodies in various methods for the detection, diagnosis and prognosis of diseases related to the aberrant expression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders such, these compositions are useful for identifying immune disorders including myasthenia gravis and multiple sclerosis, inflammatory disorders e.g. asthma and rheumatoid arthritis, infectious diseases such as AIDS and proliferative disorders including leukaemia, carcinoma and the model of the control of the co
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 activities such as antirheumatic, antiarthritic, neuroprotective antiinflammatory, antiasthmatic, antiallergic and cytostatic. The polypoptide sequence is a single chain antibody that binds BLyS invention. NOTE: The sequence data for this patent did not form I the printed specification, but was obtained in electronic format directely from WIPO at ftp.wipo.int/pub/published pct_sequences.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 259 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    This invention relates to novel antibodies that immunospecifically bind
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BLys), useful for detecting rheumatoid arthritis, asthma
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to B lymphocyte stimulator (BLyS). The BLyS gene has been mapped to concorosine 13q34 and encodes a protein that is a member of the tumour concorosine factor superfamily and induces both in vivo and in vitro B cell cyroliferation and differentiation. Specifically, it refers to single chain antibody molecules (scFvs) derived, preferably, from the variable chavy CDR3 region that immunospecifically bind to a polypeptide, or cragment thereof, of either human, murine, rat or monkey BLyS. The cyrosent invention refers to the use of such antibodies in various methods coronate spression or inappropriate function of BLyS or its receptor. As such, these compositions are useful for identifying immune disorders concluding myasthenia gravis and multiple sclerosis, inflammatory concluders e.g. asthma and rheumatoid arthritis, infectious diseases such concluding diseases such and spropriate sclerosis, inflammatory considers e.g. asthma and rheumatoid arthritis, infectious diseases such a AIDS and proliferative disorders including leukaemia, carcinoma and considers e.g. asthma and chematoid arthritis, infectious diseases such a AIDS and proliferative disorders including leukaemia, carcinoma and considers including various and multiple sclerosis.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MS,
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Best Local S
Matches 20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; NKG2D; NKG2D receptor complex; cancer; infectious disease; tumour; autoimmune disease; head; neck; stomach; oesophagus; colon; liver; ovary; intrahepatic bile duct; pancrease; lung; larynx; breast; uterus; cervix; prostate; kidney; testis; thyroid; bladder; brain; melanoma; myeloma; Fv; sarcoma; leukaemia; lymphoma; virus; bacterium; fungus; protozoan; DAP10; helminth; cytostatic; antimicrobial; immunomodulatory; 1182D10; 6H7E7; 8G7C10; 6ESA7; 1182D104-7; 8G7C104-7; 6ESA7x4-7; P4-2; P4-3; P4-14; P4-15; P5-2; P5-3; P5-9; P5-10; P5-11; P5-3; 3B10xP4-3; 3B10xP4-14; P4-15; P5-2; P5-3; P5-10; P5-11; P5-3; 3B10xP4-3; 3B10xP4-14;
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Mayer
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                                                                                                                                                                                                                                                                                                                                                                                      Multifunctional polypeptides comprising binding sites that specifically recognize extracellular groups of the NKG2D receptor complex and domain which function as receptors or ligands, useful for treating cancers and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2002-055119/07.
N-PSDB; AAS97136.
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The invention relates to a multifunctional polypeptide comprising a domain with a binding site that specifically recognises an extracellul group of the NKG2D receptor complex and a second domain which function as a receptor or ligand. The polypeptide and its associated polynucleotide are used for the preparation of a pharmaceutical composition for the treatment of cancer, infections and/or autoimmune conditions. The cancer may be a tumour of the head and neck, stomach, esophagus, colon, liver, intrahepatic bile ducts, pancreas, lung, larynx, breast, ovary, uterus, cervix, prostate, kidney, testis, thyre

extracellular

functions

thyroid,

breast, ovary, or brain, or a

Example

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Fig 16; 114pp; English.

infectious diseases.

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The infectious diseases can be caused by viruses, bacteria, fungi, CC protozoa or helminths. The autoimmune diseases include multiple CC sclerosis, Grave's disease, ankylosing spondylitis, acute anterior CC uveitis, Goodpasture's syndrome, myasthenia gravis, insulin-dependent CC diabetes mellitus, rheumatoid arthritis, pemphigus vulgaris and CC autoimmune hepatitis. Sequences ANUT2820-ANUT2875 represent the NKG2D CC receptor and the polypeptides of the invention XX Sequence 259 AA;

Query Match 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 18; Conservative 0; Mismatches 0; Indels 0; Gaps 0; Matches 18; GGGGSGGGGSEL 145

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US-08-468-609A-141
US-08-46-872A-141
US-08-762-227A-141
US-09-632-570-5
US-09-632-570-5
US-09-632-570-3
US-09-079-723-228
US-09-079-723-228
US-09-079-723-243
US-09-079-723-243
US-09-419-788-114
US-09-195-8598-4
US-08-468-609A-133
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Sequence 111, App
Sequence 141, App
Sequence 35, Appl
Sequence 35, Appl
Sequence 228, App
Sequence 236, App
Sequence 236, App
Sequence 243, App
Sequence 243, App
Sequence 241, App
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US-09-949-016-10093	US-09-949-016-9267	US-09-248-796A-20465	US-09-248-796A-18507	US-09-248-796A-15939	US-09-919-039-109	US-09-270-767-33541	US-09-602-787A-476	US-09-071-252-9	US-09-976-594-229	US-09-445-774-27	US-09-489-039A-9829	US-09-742-693-33	US-09-252-991A-30105	US-09-252-991A-28573	US-09-252-991A-25689	US-08-762-227A-155	US-08-762-227A-133
Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence	Sequence
10093, A	9267, Ap	20465, A	18507, A	15939, A	109, App	33541, A	476, App	9, Appli	229, App	27, Appl	9829, Ap	33, Appl	30105, A	28573, A	25689, A	155, App	133, App

ALIGNMENTS

TITLE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease ; TITLE OF INVENTION: Resistance ; FILE REFERENCE: 0147-0189P ; CURRENT APPLICATION NUMBER: US/09/419,788 ; CURRENT FILING DATE: 1999-10-18 ; EARLIER APPLICATION NUMBER: 98 11 9630.6 EP ; EARLIER FILING DATE: 1998-10-16 ; EARLIER FILING DATE: 1998-10-16 ; EARLIER FILING DATE: 1998-10-16 ; MUMBER OF SEQ ID NOS: 163 ; SOFTWARE: Patentin Ver. 2.1 ; SEQ ID NO 29 ; LENGTH: 259 ; TYPE: PRT ; ORGANISM: Artificial Sequence ; FEATURE: COTURE: TOTALED THEORY AND SET OF ARTIFICIAL Sequence (PARTURE); PRODUNTION DESCRIPTION OF ARTIFICIAL SEQUENCE (PARTURE); PR GENERAL INFORMATION: APPLICANT: FISCHER, Rainer APPLICANT: SCHILLBERG, Stefan APPLICANT: NAHRING, JORG APPLICANT: NAHRING, JORG APPLICANT: MONECKE, Michael APPLICANT: LIAO, Yu-Cai APPLICANT: SPIEGEL, Holger APPLICANT: SPIEGEL, Holger APPLICANT: EMANS, Neil RESULT 1 US-09-419-788-29 RESULT 2 US-09-419-788-115 멍 á US-09-419-788-29 Sequence 29, Appli Patent No. 6825325 Matches Query Match OTHER INFORMATION: Description of Artificial Sequence: OTHER INFORMATION: natural origin Local 116 seegeseegeseges 128 seeeeseeseeses 143 16; Similarity Application US/09419788 Conservative 100.0%; Stefan 6.2%; Score 16; [00.0%; Pred. No. <u>.</u> Mismatches DB 4; L 2.4e-05; 0 Length 259; Indels synthetic, ٥, Gaps

Sequence 115, Application US/09419788
Patent No. 6825325
GENERAL INFORMATION:
APPLICANT: FISCHER, Rainer
APPLICANT: SCHILLBERG, Stefan

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Best Local Similarity 100.0%; P
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SEQ ID NO 115
LENGTH: 259
TYPE: PRT
                                                                   Matches
                                                                                                   Query Match
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EARLIER APPLICATION NUMBER: 66/BOM/1998 INDIA
EARLIER FILING DATE: 1998-10-16
NUMBER OF SEQ ID NOS: 163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION NUMBER: US/09/419,788
CURRENT FILING DATE: 1999-10-18
EARLIER APPLICATION NUMBER: 98 11 9630.6 EP
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IIILE OF INVENTION: Resistance
FILE REFERENCE: 0147-0189P
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APPLICANT: ZIMMERMAN, Sabine
APPLICANT: EMANS, Neil
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APPLICANT: SACK, Markus
APPLICANT: MONECKE, Michael
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[NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                    MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/469,318
                                                                                                                                                                                                                                                                                    CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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TITLE OF INVENTION: Pro
NUMBER OF SEQUENCES: 1:
COMPUTER READABLE FORM:
                                                                                                                                                   MOLECULE TYPE: protein
                                                                                                                                                                 STRANDEDNESS
TOPOLOGY: 1
                                                                 Local Similarity 100 les 7; Conservative
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GGGSGGG 129
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Pred. No.
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; Sequence 5, Application US/09216295; Patent NO. 6268328; GENERAL INFORMATION: APPLICANT: Mitchinson, Colin APPLICANT: Wendt, Dan J. APPLICANT: WENDTION: NO. 6268328el V. FILE REFERENCE: GC555
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Best Local Similarity
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                                                                                                       RESULT 5
US-09-216-295-5
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Patent No. 60
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SEQUENCE CHARACTERISTICS:
LENGTH: 259 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08.
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,5
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/468,609A
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CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                             STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                              TYPE: amino acid
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CLASSIFICATION:
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INVENTION: Fusion Proteins Comprising Multiply Mutated Inteleukin-3 (IL-
SEQUENCES: 197
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Paik, Kumnan
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Klein, Barbara K.
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Braford-Goldberg,
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   N: No. 6268328el Variant EGIII-Like Cellulase Compositions
GC555
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Peter O.
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CURRENT APPLICATION NUMBER: US/09/216,295
CURRENT FILING DATE: 1998-12-18
NUMBER OF SEQ ID NOS: 41
SOFTWARE: FASKSEQ for Windows Version 3.0
SEQ ID NO 5
LENGTH: 259
TYPE: PRT
ORGANISM: Aspergillus aculeatus
US-09-216-295-5
; TOPOLOGY: 1:
; MOLECULE TYPE:
US-08-446-872A-141
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US-08-446-872A-141
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Ver
CURRENT APPLICATION NUMBER: US/08/446,872A
FILING DATE: 06-UUN-1995
CLASSIFICATION DATA:
APPLICATION TOMBER: US 08/192,325
FILING DATE: 14-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION: APPLICANT: Abrams,
                                                                                                            SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis TITLE OF INVENTION: Fusion Protein NUMBER OF SEQUENCES: 197
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APPLICANT:
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                                                                                                                                                                                                   NAME: Bennett, Dennis A. REGISTRATION NUMBER: 34,547 REFERENCE/DOCKET NUMBER: C-:
                                                  STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ADDRESSEE: Dennis A. Bennett, G.D. ADDRESSEE: Corporate Patent Dept. STREET: P. O. Box 5110
                                                                       TYPE: amino acid
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                                                                                        LENGTH:
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                                                                                          259 amino acids
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Paik, Kumnan
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Bauer, S. C.
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Pred. No. 4.5e+02;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length 259;
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MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO: 141:
US-08-762-227A-141
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US-08-762-227A-141
                                                           Query Match
Best Local Similarity
Matches 7; Conserv
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Matches
                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 141: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/762,227A
FILING DATE: 09-Dec-1996
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Bennett, Dennis A.
REGISTRATION NUMBER: 34,547
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ZIP: 60680
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                               TELEFAX: (708)470-6881
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
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TITLE OF INVENTION: Multivariant IL-3 Hematopoiesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES: 197
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Abrams,
                               130 GGGSGGG 136
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123 GGGSGGG 129
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                                                                                                                                                                                               LENGTH: 259 amino acids
TYPE: amino acid
STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US 08/192,325
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: US 08/446,872
FILING DATE: 06-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STREET: P. O. Box 5110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Dennis A. Bennett, G.D. Searle & Co., Corporate Patent Dept.
                                                                                                                                                                                   ΓΟΡΟLOGY: linear
                                                              2.7%; So ilarity 100.0%; I Conservative 0;
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Olins, Peter O.
Paik, Kumnan
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Maire H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Caparon, Maire H.
Easton, Alan M.
Klein, Barbara K.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Fusion Protein
                                                                ; Score 7; DB 4
b; Pred. No. 4.5
0; Mismatches
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o. 4.5e+02;
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                                                                                               Length 259
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; TYPE: PRT ; ORGANISM: Aspergillus aculeatus US-09-632-575-35
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PCT-US95-01185-141
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US-09-632-575-35
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Patent No. 6635465

GENERAL INFORMATION:
APPLICANT: Gualfetti, Peter
APPLICANT: Mitchinson, Colin
APPLICANT: Mitchinson, Colin
APPLICANT: Mopp, Traci M.
TITLE OF INVENTION: Mutant EGIII Cellulase, DNA Encoding
TITLE OF INVENTION: Such EGIII Compositions and Methods for Obtaining Same
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Best Local Similarity 100.0%; P
7. Conservative 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CURRENT APPLICATION NUMBER: US/09/632,575
CURRENT FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 54
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOPTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 5
LENGTH: 259
TYPE: PRT
ORGANISM: Aspergillus aculeatus
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APPLICANT: Gualfetti, Peter
APPLICANT: Mitchinson, Colin
APPLICANT: Phillips, Jay Ian
TITLE OF INVENTION: No. 6623949el Variant EGIII-Like Cellulase
TITLE OF INVENTION: Compositions
FILE REFERENCE: GC631
                                                                                                                                          Sequence 141, Application PC/TUS9501185 GENERAL INFORMATION:
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Best Local :
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CURRENT FILING DATE: 2000-08-04
NUMBER OF SEQ ID NOS: 64
TITLE OF INVENTION: Multivarian
TITLE OF INVENTION: Protein
NUMBER OF SEQUENCES: 196
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 259
                                                                                                                            APPLICANT:
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Local Similarity 100.0%;
hes 7; Conservation
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                                                                                                     Multivariant IL-3 Hematopoiesis Fusion
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; Pred. No. 4.5e+02;
0; Mismatches 0;
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o. 4.5e+02;
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Best Local Similarity
Matches 7; Conserv
                                                                                                                                                                                                                         COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: RastSEQ Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,7
FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US 0
FILING DATE: 14-FEB-1994
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
                                            INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 259 amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
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APPLICANT:
                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Cagney, Gerard M.
APPLICANT: Belinka, Benjamin A.
APPLICANT: Carter, John M.
APPLICANT: Carter, John M.
TITLE OF INVENTION: RANDOM PEPTIDES THAT BIND TO GASTRO-
TITLE OF INVENTION: INTESTINAL TRACT (GIT) TRANSPORT RECEPTORS AND RELATED METHODS
NUMBER OF SEQUENCES: 265
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT:
APPLICANT:
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SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: New York
STATE: New York
              STRANDEDNESS:
                                                                                                               TELEPHONE: 212-790-9090
TELEFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                           COUNTRY:
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TYPE: amino acid
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                               TYPE: amino acid
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                                                                                                 66141 PENNIE
                                               259 amino acids
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O'Mahony, Daniel J.
Lambkin, Imelda J.
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unknown
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100.0%;
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0; Mismatches
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o. 4.5e+02
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RESULT 13
US-09-079-723-243
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US-09-079-723-236
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Sequence 243,
                                                                                                                         Matches
                                                                                                                                                 Query Match
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                                                                                                                                                                                                                                                                TELEX: 66141 PENNIE
NFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: FastSEQ Version 2.0 CURRENT APPLICATION DATA:
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MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 2
                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 212-790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE OF INVENTION: RANDOM PEPTIDES THAT BIND TO GASTRO-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT:
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                                                                                                                  Match
Local Similarity 100.0%; Pred. No. 2...
Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                   NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER: IBM Compatible OPERATING SYSTEM: DOS SOFTWARE: FastSEQ Version
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET:
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Local Similarity 100.0%; P
nes 6; Conservative 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: US/09/079,723 FILING DATE:
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                                                                                                                                                                                                                                                                                                       TELEFAX:
                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION:
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                                                                                             253 LVPRGS 258
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                                                                                                                                                                                                                                     amino acid
                                                                     LVPRGS 226
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1155 Avenue of the Americas
Application US/09079723
                                                                                                                                                                                                                                                   259 amino acids
                                                                                                                                                                                                                                                                                                          212-869-9741
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Belinka, Benjamin A.
Carter, John M.
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Lambkin, Imelda J.
Singleton, Judith
Patterson, Catherine A.
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3. 2.9e+03;

ches 0; Indels
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                                                                                                                                                    Length 259;
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US-09-079-723-248
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                                                                                                                                                                                                                        GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION UNMER: 18,872
REFERENCE/DOCKET NUMBER: 1101
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9990
TELEPFAX: 212-869-9741
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       INFORMATION FOR SEQ ID NO:
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APPLICANT:
APPLICANT:
                                            APPLICANT: Cagney, Gerard M.
APPLICANT: Belinka, Benjamin A.
APPLICANT: Carter, John M.
TITLE OF INVENTION: RANDOM PEPT!
TITLE OF INVENTION: INTESTINAL 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 2.0
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
LENGTH: 259 amino acid
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MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
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                NUMBER OF SEQUENCES: 2
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STATE: New Yor
                                                                                                                                                                                                                                                                                                                                                                                                               Local Similarity tes 6; Conserv
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ZIP: 10036
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ADDRESSEE:
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Carter, John M.
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Patterson, Catherine
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Lambkin, Imelda J.
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Lambkin, Imelda J.
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Pennie & Edmonds LLP
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                              RANDOM PEPTIDES THAT BIND TO GASTRO-
INTESTINAL TRACT (GIT) TRANSPORT RECEPTORS AND RELATED METHODS
265
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INTESTINAL TRACT (GIT) TRANSPORT RECEPTORS AND RELATED METHODS
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COUNTRY: USA ZIP: 10036

T: 1155 Avenue of the Americas New York : New York

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APPLICANT: ZIMMERWAN, Sabine
APPLICANT: ZIMMERWAN, Sabine
APPLICANT: ZIMMERWAN, Sabine
APPLICANT: EMANS, Neil
ITILE OF INVENTION: Molecular Pathogenicide Mediated Plant Disease
ITILE OF INVENTION: Resistance
FILE REFERENCE: 0147-0189P
CURRENT APPLICATION NUMBER: US/09/419,788
CURRENT FILING DATE: 1999-10-18
EARLIER FILING DATE: 1999-10-18
EARLIER FILING DATE: 1998-10-16
EARLIER FILING DATE: 1998-10-16
EARLIER FILING DATE: 1998-10-16
INUMBER OF SEQ ID NOS: 163
SOPTWARE: Patentin Ver. 2.1
SEQ ID NO 114
LENGTH: 259
TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
ORGANISM: Artificial Sequence
; OTHER INFORMATION: Description of Artificial Sequence: synthetic, no
; OTHER INFORMATION: natural origin
US-09-419-788-114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: FISCHER, Rainer
APPLICANT: SCHILLBERG, Stefan
APPLICANT: NAHRING, JORG
APPLICANT: NAHRING, JORG
APPLICANT: MONECKE, Michael
APPLICANT: HONECKE, Michael
APPLICANT: LIAO, Yu-Cai
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      В
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TOPOLOGY: unknown

MOLECULE TYPE: peptide
US-09-079-723-248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: 212-869-9741
TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 259 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 114, Application US/09419788 Patent No. 6825325
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match 2.3%; Score 6; DB Best Local Similarity 100.0%; Pred. No. 2. Matches 6; Conservative 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       REFERENCE/DOCKET NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 110
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-790-9090
TELEPAX: 212-869-9741
TELEX: 66141 pproximation
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OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ Version 2.0
CURRINT APPLICATION DATA:
APPLICATION NUMBER: US/09/079,723
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskette
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No. 2.9e+03; Indels
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Search completed: September 26, 2005, 13:16:25 Job time : 42 secs

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Result
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Maximum DB
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Word size :
                                                                                                                                                                                                                                                                                           Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                            Score
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq length: 259 seq length: 259
     Query
Match
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259
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Copyright (c) 1993 - 2005 Compugen Ltd
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/ cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*
/ cgn2_6/ptodata/2/pubpaa/US09E_PUBCOMB.pep:*
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   _6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
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6/ptodata/2/pubpaa/PCT NEW PUB.pep:*
6/ptodata/2/pubpaa/US06 NEW PUB.pep:*
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US-10-863-729-18
US-09-880-748-1034
US-10-293-418-1034
US-09-880-748-1263
US-09-880-748-1263
US-09-880-748-1270
US-09-880-748-1270
US-09-880-748-1275
US-09-880-748-1497
US-10-293-418-1247
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Sequence
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Sequence
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Sequence
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 1034, Ap
1034, Ap
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1247, Ap
1263, Ap
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1197, Ap
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 18, Application US/10863729
Publication No. US20050013819A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                              PRIOR FILING DATE: 2003-09-16
NUMBER OF SEQ ID NOS: 32
SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 18
LENGTH: 259
                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                           APPLICANT: Carles-Kinch, Kelly
APPLICANT: Kinch, Michael S.
TITLE OF INVENTION: USE OF EphA4 AND MODULATOR OF EphA4 FOR
TITLE OF INVENTION: DIACNOSIS, TREATMENT AND PREVENTION OF CANCER
FILE REFERENCE: 10271-117-99
CURRENT APPLICATION NUMBER: 08/10/863,729
CURRENT FILING DATE: 2004-06-07
PRIOR APPLICATION NUMBER: 60/476,909
PRIOR APPLICATION NUMBER: 60/453,356
PRIOR APPLICATION NUMBER: 60/503,356
                                                                                                                                                                                     TYPE: PRT
ORGANISM: Homo Sapiens
FEATURE:
                                                                                            Local
                        176 LAWYQQKPGQAPRLLIYGASTRATG
164 LAWYQQKPGQAPRLLIYGASTRATG
                                                                          . Similarity
25; Conserv
                                                                        9.7%; Silarity 100.0%; Conservative 0;
                                                                        Score 25; DB; Pred. No. 3.7
  188
                                    200
                                                                                            DB 17; 1
3.7e-13;
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                                                                                                             Length 259;
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Sequence

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US-09-880-748-1034
                                                                    US-10-293-418-1034
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US-09-880-748-1034
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PRIOR FILLING DATE: 2000-06-15
PRIOR FILLING DATE: 2000-06-15
PRIOR FILLING DATE: 2000-10-17
PRIOR FILLING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276, 248
PRIOR FILLING DATE: 2001-03-16
PRIOR FILLING DATE: 2001-03-16
PRIOR FILLING DATE: 2001-03-25
PRIOR FILLING DATE: 2001-03-25
PRIOR FILLING DATE: 2001-03-25
PRIOR FILLING DATE: 2001-05-25
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SEQ ID NO 1034
LENGTH: 259
Query Match
Best Local Similarity
                                                                                                                                                          NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1034
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PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
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CURRENT FILING DATE: 2002-11-27
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind
FILE REFERENCE: PF523P2
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CURRENT FILING DATE: 2001-06-15
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                                                                                                                                                                                                         PRIOR FILING DATE:
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                                                                                     ORGANISM: Homo sapiens
                                                                                                                  LENGTH: 259
TYPE: PRT
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DR FILLING DATE: 2001-05-25
DR APPLICATION NUMBER: 60/277,379
DR FILLING DATE: 2001-03-21
DR APPLICATION NUMBER: 60/276,248
DR FILLING DATE: 2001-03-16
DR FILLING DATE: 2001-03-16
DR APPLICATION NUMBER: 60/240,816
DR FILLING DATE: 2000-10-17
DR APPLICATION NUMBER: 60/212,210
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8.1%;
100.0%;
  Score 21;
Pred. No.
  DB 15;
1e-09;
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NUMBER OF SEQ ID NOS: 3239
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 1247
LENGTH: 259
TYPE: PRI
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                                    ; ORGANISM: Homo sapiens US-09-880-748-1247
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SEQ ID NO 1043
LENGTH: 259
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Query Match
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
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PRIOR FILING DATE: 2001-05-25
NUMBER OF SEQ ID NOS: 3239
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PRIOR APPLICATION NUMBER: 60/277,379
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CURRENT FILING DATE: 2001-06-15
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
                                                                                                                                                                                                                              PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523
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7.78;
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20;
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DB 10;
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APPLICANT: Ruben et al.

APPLICANT: Ruben et al.

TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS

FILE REFERENCE: PF523

CURRENT APPLICATION NUMBER: US/09/880,748

CURRENT FILING DATE: 2001-06-15

PRIOR APPLICATION NUMBER: 60/212,210

PRIOR FILING DATE: 2000-06-15

PRIOR APPLICATION NUMBER: 60/210,816

PRIOR APPLICATION NUMBER: 60/240,816

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-16

PRIOR FILING DATE: 2001-03-21

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25
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; TYPE: PRT
; ORGANISM: Homo sapiens
US-09-880-748-1263
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                                         NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.0
SEQ ID NO 1270
LENGTH: 259
TYPE: PRT
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ORGANISM: Homo sapiens
-09-880-748-1270
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PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
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CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR FILING DATE: 2000-10-17
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NUMBER OF SEQ ID NOS: 3239
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
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100.0%; Pred. No.
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US-09-880-748-1275
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; ORGANISM: Homo sapiens
US-09-880-748-1497
                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-15
PRIOR FILING DATE: 2000-10-17
PRIOR PILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
PRIOR FILING DATE: 2001-05-25
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CURRENT APPLICATION NUMBER: US/09/880,748
CURRENT FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILLING DATE: 2000-06-15
PRIOR PILLING DATE: 2000-10-17
PRIOR PILLING DATE: 2000-10-17
PRIOR PILLING DATE: 2000-10-17
PRIOR PILLING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR FILLING DATE: 2001-03-21
PRIOR FILLING DATE: 2001-03-21
PRIOR PILLING DATE: 2001-03-21
PRIOR PILLING DATE: 2001-03-21
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                                                                                  NUMBER OF SEQ ID NOS: 3239
SOFTWARE: PatentIn Ver. 2.
SEQ ID NO 1497
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SEQ ID NO 1275
LENGTH: 259
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GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Publication No. US20 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1497, Application US/09880748 Publication No. US20030059937A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS FILE REFERENCE: PF523
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Ruben et al.
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                                                                 LENGTH: 259
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. US20030059937A1
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FILL OF INVENTION: CLURENT STATES

FULL REFERENCE: PF5.23 P2

CURRENT APPLICATION NUMBER: US/10/293,418

CURRENT FILING DATE: 2002-11-27

PRIOR APPLICATION NUMBER: 60/331,469

PRIOR FILING DATE: 2001-11-16

PRIOR APPLICATION NUMBER: 60/340,817

PRIOR FILING DATE: 2001-12-19

PRIOR APPLICATION NUMBER: 09/80,748

PRIOR FILING DATE: 2001-06-18

PRIOR FILING DATE: 2001-06-25

PRIOR APPLICATION NUMBER: 60/293,499

PRIOR FILING DATE: 2001-05-25

PRIOR APPLICATION NUMBER: 60/277,379

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21

PRIOR FILING DATE: 2001-03-21
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Best Local Similarity 100.0%; F
Matches 20; Conservative 0;
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SEQ ID NO 1043
LENGTH: 259
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Publication No. US20030223996A1
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Best Local S
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind
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CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
PRIOR APPLICATION NUMBER: 60/340,817
PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR APPLICATION NUMBER: 09/880,748
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind
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APPLICATION NUMBER: 60/212,210
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0; Mismatches
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US-10-293-418-1263
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                                                                                                                                                       RESULT 13
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Sequence 1270, Application US/10293418
Publication No. US20030223996A1
GENERAL INFORMATION:
APPLICANT: Ruben et al.
TITLE OF INVENTION: Antibodies that Immunospecifically Bind
FILE REFERENCE: PF523P2
CURRENT APPLICATION NUMBER: US/10/293,418
CURRENT FILING DATE: 2002-11-27
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Best Local S
Matches 20
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PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1263
LENGTH: 259
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Publication No. US2C
GENERAL INFORMATION:
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PRIOR FILING DATE: 2000-06-16
NUMBER OF SEQ ID NOS: 3247
SEQ ID NO 1247
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PRIOR APPLICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
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CURRENT FILING DATE: 2002-11-27
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FILING DATE: 2001-06-15
APPLICATION NUMBER: 60/293,499
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APPLICATION NUMBER: 60/331,469 FILING DATE: 2001-11-16

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; NUMBER OF SEQ ID NOS: 3247
; SEQ ID NO 1270
; LENGTH: 259
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-293-418-1270
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US-10-293-418-1275
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PRIOR FILLING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILLING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR TILING DATE: 2001-05-25
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR APPLICATION NUMBER: 60/277,379
PRIOR PILLING DATE: 2001-03-21
PRIOR APPLICATION NUMBER: 60/276,248
PRIOR FILLING DATE: 2001-03-16
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/240,816
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILLING DATE: 2000-06-16
NUMBER: 60/212,210
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PRIOR FILING DATE: 2001-03-21
PRIOR PELICATION NUMBER: 60/276,248
PRIOR PELING DATE: 2001-03-16
PRIOR PELICATION NUMBER: 60/240,816
PRIOR FILING DATE: 2000-10-17
PRIOR APPLICATION NUMBER: 60/212,210
PRIOR FILING DATE: 2000-06-16
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Matches
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SEQ ID NO 1275
LENGTH: 259
TYPE: PRT
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PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
PRIOR FILING DATE: 2001-06-15
PRIOR APPLICATION NUMBER: 60/293,499
PRIOR FILING DATE: 2001-05-25
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CURRENT FILING DATE: 2002-11-27
PRIOR APPLICATION NUMBER: 60/331,469
PRIOR FILING DATE: 2001-11-16
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF523P2
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RESULT 15
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SEQ ID NO 1497
LENGTH: 259
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                                                                                                                                                                                                                                                                                                PRIOR APPLICATION NUMBER: 60/212,210 PRIOR FILING DATE: 2000-06-16
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PRIOR FILING DATE: 2001-12-19
PRIOR APPLICATION NUMBER: 09/880,748
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CURRENT FILING DATE: 2002-11-27
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TITLE OF INVENTION: Antibodies that Immunospecifically Bind BLyS
FILE REFERENCE: PF533P2
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PRIOR APPLICATION NUMBER: 60/276,248
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PRIOR APPLICATION NUMBER: 60/293,499
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PRIOR FILING DATE: 2001-11-16
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ALIGNMENTS

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R;Ng, W.V.; Kennedy, S.P.; Mahairas, G.G.; Berquist, B.; Pan, M.; Shuk; Leithauser, B.; Keller, K.; Cruz, R.; Danson, M.J.; Hough, D.W.; Mac Jung, K.H.; Alam, M.; Freitas, T.

Proc. Natl. Acad. Sci. U.S.A. 97, 12176-12181, 2000
A.Authors: Hou, S.; Daniels, C.J.; Dennis, P.P.; Omer, A.D.; Ebhardt, A; Title: Genome sequence of Halobacterium species NRC-1.
A; Reference number: A84160; MUID:20504483; PMID:11016950
A; Accession: C94165
A; Accession: C94165
A; Accession: C94165
A; Residues: 1-259 < STO>
A;Cross-references: UNIPROT:Q9HSW3; GB:AE004437; NID:g10579699; PIDN:AAG18687.1; GSPDB:GN C;Genetics:
                                                                                                                                                                                                                                                                                                                                                          hypothetical protein Vng0049h [imported] - Halobacterium sp. NRC-1
C;Species: Halobacterium sp. NRC-1
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
C;Accession: C84165
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C84165
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A;Introns: 9/2; 231/1
C;Superfamily: Phaseolus
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submitted to the EMBL Data Library, April 1997
A;Description: The sequence of C. elegans cosmid T20B6
A;Reference number: Z18297
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            hypothetical protein T20B6.3 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 20-Sep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15126
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A;Cross-references: UNIPROT:O02049; EMBL:AF000193; NID:g1946986; PID:g1946988; PIDN:AAB5;
A;Experimental source: strain Bristol NZ; clone T20B6
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                                                                                                                                                                                                                                                                                                        G.G.; Berquist, B.; Pan, M.; Shukla, H.D.; Lasky, S.R.; Danson, M.J.; Hough, D.W.; Maddocks, D.G.; Jablor
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Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.

Nature 408, 816-820, 2000
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.

A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.

A;Reference and analysis of chromosome 1 of the plant Arabidopsis.

A;Recession: F86475
A,Accession: F86475
A,Accession: F86475
                                                                                                                                                                                                                                                                A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-259 <BLO>
A;Cross-references: UNIPROT:Q04518; GB:L04507; NID:g149170; PIDN:AAA25054.1; PID:g149171
A;Experimental source: VTT-E-74023
A;Experimental source: VTT-E-74023
                                                                                                                                                                                                                                                                                                                                                                     J. Bacteriol. 175, 1392-1404, A;Title: Characterization of t A;Reference number: A47069; MU A;Accession: C47069
                                                                                                                                                                                                                                                                                                                                                                                                                               acetolactate decarboxylase (EC 4.1.1.5) - Klebsiella terrigena (;Species: Klebsiella terrigena C;Species: Klebsiella terrigena C;Date: 10-Sep-1999 #sequence_revision 10-Sep-1999 #text_change 09-Jul-2004 C;Accession: C47069 R;Blomqvist, K.; Nikkola, M.; Lehtovaara, P.; Suihko, M.L.; Airaksinen, U.; Straby, J. Bacteriol. 175, 1392-1404, 1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Note: sequence extracted from NCBI backbone (NCBIN:126766, NCBIP:126767) C; Superfamily: acetolactate decarboxylase C; Keywords: carbon-carbon lyase; carboxy-lyase
RESULT 5
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A;Molecule type: DNA
A;Residues: 1-259 <STC
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;Species: Arabidopsis thaliana (mouse-ear cress)
;Sate: 02-Mar_2001 #sequence_revision 02-Mar-2001 #text_change 09-Jul-2004
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100.0%; Pred. No. 8.8e+02;
tive 0; Mismatches 0;
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0; Mismatches
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A;Residues: 26-259 <LUIZ>
A;Residues: 26-259 <LUIZ>
A;Residues: 228-Met was also found
A;Note: 228-Met was also found
R;Julkunen, M.; Koistinen, R.; Aalto-Setaelae, K.; Seppaelae, M.; Jaenne,
R;BS Lett. 236, 295-302, 1988
A;Title: Primary structure of human insulin-like growth factor-binding propagation of the primary structure of human insulin-like growth factor-binding propagation of the primary structure of human insulin-like growth factor-binding propagation of the primary structure of human insulin-like growth factor-binding propagation of the primary structure of human insulin-like growth factor-binding propagation of the primary structure of human insulin-like growth factor-binding propagation of the primary structure of human insulin-like growth factor-binding propagation of the primary structure of human insulin-like growth factor-binding propagation of the primary structure of human insulin-like growth factor-binding propagation of the primary structure of human insulin-like growth factor-binding propagation of the primary structure of human insulin-like growth factor-binding propagation of the primary structure of human insulin-like growth factor-binding propagation of the primary structure of human insulin-like growth factor-binding propagation of the primary structure of human insulin-like growth factor-binding propagation of the primary structure of human insulin-like growth factor-binding propagation of the primary structure of human insulin-like growth factor-binding propagation of the primary structure of human insulin-like growth factor-binding propagation of the primary structure of human insulin-like growth factor-binding propagation of the primary structure of human insulin-like growth factor-binding propagation of the primary structure of human insulin-like growth factor-binding propagation of the primary structure of human insulin-like growth factor-binding propagation of the primary structure of human insulin-like growth factor-binding propagation of the primary structure of human insuli
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A; Residues: 1-259 <LEB>
A; Residues: 1-259 <LEB>
A; Cross-references: GB: M31145; NID: g183117; PIDN: AAA52542.1; PID: g183118
A; Note: part of this sequence, including the amino end of the mature protein,
A; Note: part of this sequence, including the amino end of the mature protein,
R; Ehrenborg, E.; Larsson, C.; Stern, I.; Janson, M.; Powell, D.R.; Luthman, H.
Genomics 12, 497-502, 1992
Genomics 12, 497-502, 1992
A; Title: Contiguous localization of the genes encoding human insulin-like grow
A; Reference number: A42176; MUID: 92217971; PMID: 1373120
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A;Title: Structure of the human chromosomal gene for the 25 kl A;Reference number: A40155; MUID:89330502; PMID:2474129
A;Accession: A40155
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Povoa, G.; Hall, K.; Joernvall, H.

Eur. J. Biochem. 180, 259-265, 1989
A;Title: Human insulin-like growth-factor-binding protein. Low-molecular-mass A;Reference number: S03559; MUID:89170723; PMID:2466665
A;Accession: S43207
A;Cross-references: EMBL:X13405; NID:g35574; PIDN:CAA31771.1; R;Brewer, M.T.; Stetler, G.L.; Squires, C.H.; Thompson, R.C.; Biochem. Biophys. Res. Commun. 152, 1289-1297, 1988
A;Title: Cloning, characterization, and expression of a human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Molecule type: mRNA
A;Residues: 141-259 <LUT1>
A;Cross-references: EMBL:X15002; NID:g33013; PIDN:CAA33110.1;
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Biochem. Biophys. Res. Commun. 157, 898-907, 1988
A;Title: Organization of the gene encoding the insulin-like growth factor binding A;Reference number: A31867; MUID:89087480; PMID:2849945
                                                                                                                                                                                                               A; Molecule type: mRNA
A; Residues: 1-252, 'M', 254-259 <JUL>
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A;Residues: 174-252,'M',254-259 <EHR>
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A; Residues: 1-259 < CUB>
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A; Residues: 1-252, 'M', 254-259 <BR2>
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A; Residues: 1-259 < BRI>
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N;Alternate names: IGF-binding protein; IGF-BP25; insulin-like growth fact
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Busby, W.H.;
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                                                                                                                  Clemmons,
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of a human

insulin-like

growth

factor

132

GSGGG

136

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R;Hirose, T.; Sugita, M.; Sugiura, M.
Mol. Gen. Genet. 244, 360-366, 1994
A;Title: Characterization of a cDNA encoding a novel type
A;Reference number: S46286; MUID:94359458; PMID:8078461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Cross-references: GDB:120075; OMIM:146730
A;Map position: 7p13-7p12
A;Introns: 117/1; 173-7j:12
C;Superfamily: insulin-like growth factor binding protein; thyroglobulin C;Keywords: phosphoprotein
E;1-25/Domain: signal sequence #status predicted <SIG>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Accession: A61099
A;Molecule type: protein
A;Rosidues: 26-40,'P',42 <BEL>
C;Comment: This protein binds insulin-like growth
C;Comment: This protein is not glycosylated.
C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A;Residues: 26-53 CBUS>
R;Bell, S.C.; Keyte, J.W.
Endocrinology 123, 1202-1204, 1988
Endocrinology 123, 1202-1204, 1988
A;Title: N-terminal amino acid sequence of weight IGF binding proteins.
A;Reference number: A61099; MUID:88283527;
                                                                                                                                                                                                                                                                                                                                RNA-binding protein - wood tobacco
C;Species: Nicotiana sylvestris (wood tobacco)
C;Date: 10-Sep-1999 #sequence_revision 10-Sep-
C;Accession: S46286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X12385; NID:g35571; PIDN:CAA30942.1; PID:g35572 R;Busby Jr., W.H.; Klapper, D.G.; Clemmons, D.R. J. Biol. Chem. 263, 14203-14210, 1988
A;Title: Purification of a 31,000-Dalton insulin-like growth factor bind A;Reference number: A30804; MUID:89008261; PMID:2971653
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Residues: 1-54,'PAAAVARCAPCLWAPR',72-212,'Q',214-259 <BRE>A;Cross-references: GB.M20841; NID:9183113; PIDN:AAA52540.1; A;Note: the authors translated the codon CAG for residue 213 R;Grundmann, U.; Nerlich, C.; Bohn, H.; Rein, T. Nucleic Acids Res. 16, 8711, 1988
                                                                                        A;Cross-references: UNIPROT:Q40436; GB:D26182; NID:g575607; PIDN:BAA05170.1; PID:g62492:
C;Superfamily: wood tobacco RNA-binding protein; ribonucleoprotein repeat homology
F;41-108/Domain: ribonucleoprotein repeat homology <RRM1>
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A;Accession: A27694
A;Molecule type: mRNA
A;Residues: 1-54,'PAAAVARCAPCLWAPR',72-212,'Q',214-259
                                                                                                                                                          A; Molecule type: mRNA
A; Residues: 1-259 <HII
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                                                                                                                                                                                                      A;Status: preliminary
                                                                                                                                                                                                                            A; Accession: S46286
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    Matches
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  Similarity 5; Conserv
  Conservative 0;
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Score 5; DB 1; Pred. No. 7.4
0; Mismatches
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E55217
cis-1, 2-dihydro-1, 2-dihydroxynaphthalene dehydrogenase (EC 1.3 N;Alternate names: polycyclic aromatic hydrocarbon dihydrodiol C;Species: Pseudomonas putida
C;Species: 05-May-1995 #sequence_revision 05-May-1995 #text_change
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A;Gene: PA1330
C;Superfamily:
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Nature 406, 959-964, 2000
A;Title: Complete genome seq
A;Reference number: A82950;
                                                                                                                                                                                                                                                                                                                                     C;Accession: F83479
R;Stover, C.K.; Pham, X.Q.; Erwin, A.L.; Mizoguchi, S.D.; Warrener, adman, S.; Yuan, Y.; Brody, L.L.; Coulter, S.N.; Folger, K.R.; Kas,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              A;Gene: doxE
C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase
C;Keywords: oxidoreductase
F;5-183/Domain: short-chain alcohol dehydrogenase homology <SADH>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: DNA
A; Residues: 1-259 < DEN>
A; Cross-references: GB: M60405
C; Genetics:
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A;Status: preliminary
                                                                                                                                                                                A;Cross-references: UNIPROT:Q91414; GB:AE004562; GB:AE004091; NID:g9947263; PIDN:AAG0471:
A;Experimental source: strain PAO1
                                                                                                                                                                                                                  A; Molecule type: DNA
A; Residues: 1-259 < STO>
                                                                                                                                                                                                                                                                                                                                                                                                                        probable short-chain dehydrogenase PA1330 [imported]
C;Species: Pseudomonas aeruginosa
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       C;Date: 07-Apr-1994 #sequence_revision
C;Accession: D49343; S27635
                                                                                                                                                                                                                                                     A;Status:
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            2-dihydro-1,2-dihydroxynaphthalene dehydrogenase
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50; MUID:20437337; PMID:10984043
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No. 7.4e+03;
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A.; Larbig,
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#sequence_revision 05-May-1995 #text_change 09-Jul-2004

1.3.1.29) - Pseud diol dehydrogenase

Pseudomonas

putida

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A; KCCebsiu...A; A; KCCebsiu...A; A; Kolecule type: DNA
A; Molecule type: DNA
A; Residues: 1-259 < STO>
A; Cross-references: UNIPROT: Q9KCR3;
A; Cross-references: strain C-125
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C;Accession: E55217

R;Takizawa, N.; Kaida, N.; Torigoe, S.; Moritani, T.; Sawada, T.; Satoh, S. J. Bacteriol. 176, 2444-2449, 1994

A;Title: Identification and characterization of genes encoding polycyclic A;Acference number: A55217; MUID:94209249; PMID:8157615

A;Accession: E55217

A;Status: preliminary

A;Molecule type: DNA
A;Residues: 1-259 <TAK>
A;Cross-references: UNIPROT:Q08669; GB:AB004059; GB:D16629; NID:g2189972; C;Genetics:
A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1.
A;Reference number: A75250; MUID:20036896; PMID:10567266
A;Accession: C75410
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-259 <WHI>A;Residues: 1-259 <WHI>A;Cross-references: UNIPROT:Q9RUS1; GB:AE001978; GB:AE000513; NID:g6459059; PIDN:AAF1088
A;Experimental source: strain R1
C;Genetics:
                                                                                                                                                                                                                                                                                                                                      methionine aminopeptidase - Deinococcus radiodurans (strain R1)
c;Species: Deinococcus radiodurans
C;Date: 03-Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-00;Accession: C75410
C;Accession: C75410
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A;Title: Complete genome sequence of the alkaliphilic bacterium Bacillus halodurans A;Reference number: A83650; MUID:20512582; PMID:11058132
A;Accession: B83938
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C;Superfamily: ribitol dehydrogenase; short-chain alcohol dehydrogenase
C;Keywords: oxidoreductase
F;5-183/Domain: short-chain alcohol dehydrogenase homology <SADH>
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C;Superfamily: ribitol dehydrogenase; short-chain alcohol
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0; Mismatches
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5. 7.4e+03;
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T.; Zalewski,
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A;Residues: 1-259 <RES>
A;Cross-references: GB:M25792; NID:g576810; PIDN:AAA53439
C;Genetics:
A;Gene: pgp3
A;Introns: 66/3; 142/3; 191/3
C;Superfamily: multidrug resistance protein; ATP-binding C;Superfamily: nucleotide binding; P-loop C;Keywords: ATP- nucleotide binding; P-loop P;25-228/Domain: ATP-binding cassette homology <ABC2>
F;42-49/Region: nucleotide-binding motif A (P-loop)
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A; Introns: 22/1; 116/1;
C; Superfamily: class II
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                                                                                                                                                                                                                                                                                A;Title: Identification of members of the P-glycoprotein multigene family. A;Reference number: I48119; MUID:89261726; PMID:2566908 A;Accession: I48119
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Mol. Cell. Biol. 9, 1224-1232, 1989
                                                                                                                                                                                                                                                                                                                                                                         P-glycoprotein - Chinese hamster (fragment)
C;Species: Cricetulus griseus (Chinese hamster)
C;Date: 04-Sep-1997 #sequence_revision 04-Sep-1997 #text_change 02-Feb-2001
C;Date: 148119
C;A-Cession: [148119]
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A; Residues: 1-259 <MIL>
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R;Milne, S.; Kaufman,
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C;Species: Gallus gallus (chicken)
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 20-Jun-2000
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A; Map position:
C; Superfamily:
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                   Query Match
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erences: GB:M25792; NID:g576810; PIDN:AAA53439.1;
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ilarity 100.0%;
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                   1.9%; Score 5; |
100.0%; Pred. No.
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100.0%; Pred. No.
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o. 7.4e+03;
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o. 7.4e+03;
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probable nitrogen regulator - Deinococcus radiodurans (strain R1)
(;Species: Deinococcus radiodurans
(;Species: Deinococcus radiodurans
(;Date: 03.Dec-1999 #sequence_revision 03-Dec-1999 #text_change 09-Jul-2004
C;Accession: D75372
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; Hickey, E.K.; Peterson, J.D.; Dodson, R.J.;
R;White, O.; Eisen, J.A.; Heidelberg, J.F.; McDonald, L.; Utterback, T.; Zalewski, C.; Ma S.; Smith, H.O.; Venter, J.C.; Fraser, C.M.
Science 286, 1571-1577, 1999
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A;Gene: YPO2944
C;Superfamily: chaperone protein papD
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C;Species: Yersinia poetis
C;Date: 02-Nov-2001 #sequence_revision 02-Nov-2001 #text_change 09-Jul-2004
C;Accession: AC0358
C;Accession: AC0358
R;Parkhill, J.; Wren, B.W.; Thomson, N.R.; Titball, R.W.; Holden, M.T.G.; Prentice, M.B. deno-Tarraga, A.M.; Chillingworth, T.; Cronin, A.; Davies, R.M.; Davis, P.; Dougan, G.; il, M.; Rutherford, K.; Simmonds, M.; Skelton, J.; Stevens, K.; Whitehead, S.; Barrell, Nature 413, 523-527, 2001
                                                                                                                                                                                                                                                                                                                 A;Gene: DR1646
A;Map position: 1
C;Superfamily: regulatory protein fnr; cAMP receptor protein cyclic nucleotide-binding
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: Genome sequence of the radioresistant bacterium Deinococcus radiodurans R1. A;Reference number: A75250; MUID:20036896; PMID:10567266 A;Accession: D75372
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A;Molecule type: DNA
A;Residues: 1-259 <KUR>
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A;Molecule type: DNA
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Search completed: September 26, 2005, 13:15:37 Job time : 41 secs
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GO; GO:0008757; F:S-adenosylmethionine-dependent methyltransf.
InterPro; IPR006342; FkbM mtfrase.
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Maddocks D.G., Jablonnie, E., Krebs M.P., Angevine C.M., Dale H.,
Isenbarger T.A., Peck R.F., Pohlschroder M., Spudich J.L., Jung K.-H.,
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"Genome sequence of Halobacterium species NRC-1.";
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Cifuentes-Diaz C., Bitoun M., Goudo
Rieger F., Perin J.P., Alliel P.M.;
"Neuromuscular expression of the BT
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Alliel P.M., Seddiqi N., Goudou D., Cifuentes-Diaz C., Romero
Velasco E., Rieger F., Perin J.P.;
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GO; GO:0005515; F:protein binding;
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RESULT
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Best Local Similarity
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01-MAY-2000
01-OCT-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         InterPro; IPR002952; Eggshell.
PRINTS; PR01228; EGGSHELL.
Hypothetical protein.
SEQUENCE 259 AA; 23054 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Waterston
Submitted
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Beck C., Wamsley P.;

"The sequence of C. elegans
"The sequence of C. the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (SEP-2004) to the EMBL; AF000193; AAB52890.1; PIR; T15126; T15126.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Caenorhabditis elegans.
Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea; Rhabditidae; Peloderinae; Caenorhabditis.
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01-UTL-1997 (TYEMBLEE). 04, Last sequence update)
01-UTN-2003 (TYEMBLEE). 24, Last annotation update)
Hypothetical protein T20B6.3.
                                                                   Drosophila melanogaster (Fruit fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygo
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
Ephydroidea; Drosophilidae; Drosophila.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      "Genome sequence of the nematode C. elegans: a platform investigating biology. The C. elegans Sequencing Consort Science 282:2012-2018(1998).
                                                                                                                                                               ORFNames=CG30042;
                                                                                                                                                                                       CG30042-PA.
                                                                                                                                                                                                                                                                                                         Q9V6A4
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WormPep; T20B6.3; CE13778.
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MEDLINE=99069613; PubMed=9851916;
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    SEQUENCE
                                           NCBI_TaxID=7227;
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EMBL/GenBank/DDBJ databases.
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RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Goalyne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Goalyne J.D.,
RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Goalyne J.D.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
RA George R.C., Deven J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Batton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
RA Batton R.C., Rogers Y.H., Blazej R.G., Change M., Pfelifer B.D.,
RA Ballew R.M., Basu A., Barker E.G., Helt G., Nelson C.R., Gebor G.L.,
RA Ballew R.M., Basu A., Barker B.G., Helt G., Nelson C.R., Gebor G.L.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Borkova D., Botchan M.R., Bouck J., Brokstein P., Brottier P.,
RA Bordon K.Y. Doup L.B., Downes M., Digan-Rocha S., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Cherry J.M., Cawley S., Dahlke C., Davenport L.B., Davies P.,
RA Dodson K., Doup L.E., Downes M., Dugan-Rocha S., Dunkov B.C., Dunn P.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Harris N.L., Harvey D., Heiman T.J., Hernandez J.R., Houck J.,
RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,
RA Merkulov G., Milshina N.V., Saunders R.D., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H.,
RA Shen B., Nother R., Mor
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SEQUENCE FROM N.A.
SEQUENCE FROM N.A.
MEDLINE=22426070; PubMed=12537573;
Kaminker J.S., Bergman C.M., Kronmiller B., Ca
Kaminker J.S., Bergman C.M., Lewis S.E.,
                                                                                                                                                        MEDLINE-2242606; PubMed=12537572;

MISTA S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,

Misra S., Crosby M.A., Mungall C.J., Millburn G.H., Prochnik S.E.,

Smith C.D., Tupy J.L., Whitfied E.J., Bayraktaroglu L., Berman B.P.

Bettencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A.,

Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,

Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; "Finishing a whole-genome shotgun: Release 3 of the Drosophila melanogaster euchtomatic genome sequence."; Genome Biol. 3:RESEARCH0079-RESEARCH0079(2002).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22426065; PubMed=12537568; Carlson J.W., Halper Celniker S.E., Wheeler D.A., Krommiller B., Carlson J.W., Halper Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., George R.A., Hoskins R.A., Laverty T., Muzny D.M., Nelson C.R., George R.A., Hoskins R.A., Laverty T., Minkowski S., Sodergren E.J. Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Vent Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,
                                        systematic review."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The transposable elements of the Drosophila melanogaster euchromatin:
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    Biol.
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3:RESEARCH0083-RESEARCH0083 (2002).
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., Rubin G.M
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Oryza sativa (japonica cultivar-group).
Bukaryota; Viridiplantae; Streptophyta; Embryophyt
Spermatophyta; Magnoliophyta; Liliopsida; Poales;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.

SEQUENCE FROM N.A.

PubMed=15069639; DOI=10.1007/800438-004-1006-8;

Soranzo N., Sari Gorla M., Mizzi L., De Toma G., Frova C.;

Soranzo N., Sari Gorla M., Mizzi L., De Toma G., Frova C.;
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25-OCT-2004 (TrEMBLrel. 28
Glutathione S-transferase.
                                                                                                                                                                                                                                                      EMBL; AY541763; AAS93256.1; EMBL; AP003569; BAD37467.1;
                                                                                                                                                                                                                                                                                                                      "Oryza sativa nipponbare clone:P0425F05.";
                                                                                                                                                                                                                                                                                                                                                                                                                             transferase gene family.";
Mol. Genet. Genomics 271:511-521(2004)
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05-JUL-2004
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PROSITE; PS00867; CPSASE 2; UNKNOWN 1.

PROSITE; PS00233; CUTICLE; UNKNOWN 1
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FlyBase; FBgn0050045; CG30045
GO; GO:0042302; F:structural c
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EMBL; AE003822; AAF58524.2;
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InterPro; IPR004045;
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  QAPRLL
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                                                                                                                                                                     GST_N;
    190
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                                                                                                                               MW;
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W; ED2A2B6758EF1FD0 CRC64;
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                                                                                 Score 6;
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Pred. No.
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o. 4e+03;
                                                                                     DB
                                                                                                                                                                                                                                       IEA
                                                                  4e+03;
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Best Local S
Matches 6
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Q7XZH0;
01-OCT-2003
01-OCT-2003
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Q6ZGS2;
05-JUL-2004
05-JUL-2004
                                                                                            SEQUENCE FROM N.A.

Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M.

Buell C.R., Yuan Q., Tsitrin T., Kim M.M., Bera J.J., Jin S.S.,

Padrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S.

Yanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V.,

Yang Q.Q., Haas B.J., B.B., Peterson J.J., Quackenbush J.,

White Q., Saliberg S.L., Fraser C.M.;

"Oryza sativa chromosome 3 BAC OSJNBa0028E23 genomic sequence.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Name=OSJNBb0033J23.5; Synonyms=OSJNBa0028F23.3; Oryza sativa (japonica cultivar-group). Oryza sativa (japonica cultivar-group). Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.
     SEQUENCE
Buell R.;
                                                                                                                                                                                                                                                                                                                                                                                                                                 Buell C.R., Yuan Q., Ouyang S., Liu J., Gansberger K., Jones K.M. Overton II L.L., Tsitrin T., Kim M.M., Bera J.J., Jin S.S., Fadrosh D.W., Tallon L.J., Koo H., Zismann V., Hsiao J., Blunt S. Vanaken S.S., Riedmuller S.B., Utterback T.T., Feldblyum T.V., Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., Quackenbush J., White O., Salzberg S.L., Fraser C.M.; Submitted (NOV-2002) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant disease resistance polyprotein-like.
Name=071148 D05.10;
Oryza sativā (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
MCBI TaxID=39947;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hypothetical protein OSJNBb0033J23.5 OSJNBa0028F23.3).
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Submitted (AUG-2001)
EMBL; AP004118; BAD07
                                                                               Submitted (OCT-2002)
                                                                                                                                                                                                                                                                                                                                    Submitted
                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NCBI_TaxID=39947;
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                          FROM N.A
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (TrEMBLrel. 25, Created)
(TrEMBLrel. 25, Last sequence update)
(TrEMBLrel. 28, Last annotation updat
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(TrEMBLrel. 27,
(TrEMBLrel. 27,
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-2001) to the
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                                                                            BAC OSJNBa0028F23 genomic sequence." EMBL/GenBank/DDBJ databases.
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Last annotation update)
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Pred. No
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Best Local S
Matches 6
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Best Local S
Matches 6
                                                                                                                                                                                Q9C8P8 PRELIMINARY; PRT; 259 AA.
Q9C8P8,
Q1-JUN-2001 (TrEMBLrel. 17, Created)
O1-JUN-2001 (TrEMBLrel. 17, Last sequence update)
O5-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Helix-loop-helix protein 1A, putative; 28707-26892
(Putative bHLH transcription factor).
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SEQUENCE 259 AA; 28114 MW; 1805F80A7CEBD52
Arabidopsis thaliana (Mouse-Gaz Laura, Embryophyta;
Eukaryota; Viridiplantae; Streptophyta; Embryophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eu
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Buell C.R., Yuan Q., Ouyang S., Liu J., Gansber Overton II L.L., Tsitrin T., Kim M.M., Bera J.J Fadrosh D.M., Tallon L.J., Koo H., Zismann V., Vanaken S.S., Riedmuller S.B., Utterback T.T., Yang Q.Q., Haas B.J., Suh B.B., Peterson J.J., White O., Salzberg S.L., Fraser C.M., Submitted (JUN-2002) to the EMBL/GenBank/DDBJ d
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01-JUN-2003 (TrEMBLrel. 24, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last sequence update)
01-MAR-2004 (TrEMBLrel. 26, Last anotation update)
Hypochetical protein OSJNBb0021P10.5.
Name-OSJNBb0021P10.5;
Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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Q851D7;
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PF07320; Hin1; 1.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GGGSGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         259 AA; 27972 MW;
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ilarity 100.0%;
Conservative
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Pred. No
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o. 4e+03;
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Bera J.J., Jin
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                                                                       eudicots; rosids;
                                                                                                                                                                                                                                      (At1g35460/F12A4_2)
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RESULT 11
Q9FS62
ID Q9FS6
AC Q9FS6
DT 01-MAR
DT 01-MAR
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Best Local S
Matches 6
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Q9FS62
Q9FS62;
01-MAR-2001
01-MAR-2001
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Bowser L., Carninci P., Chang E., Dale J.M., Goldsmith A.D.,
Hayashizaki Y., Ishida J., Jones T., Kamiya A., Karlin-Neumann G.,
Kawai J., Lam B., Lee J.M., Lin J., Miranda M., Narusaka M.,
Nguyen M., Onodera C.S., Palm C.J., Quach H.L., Sakurai T., Satou Seki M., Southwick A., Tang C.C., Toriumi M., Wu H.C., Yamada K.,
Yamamura Y., Yu G., Yu S., Shinozaki K., Davis R.W., Theologis A.,
Ecker J.R.;
                                                                                                                                                                                                                                               PROSITE;
SEQUENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Shinn P., Chen H., Cheuk R., Kim C.J., Koesema E., Meyers M.C., Banh J., Bowser L., Carninci P., Dale J.M., Goldsmith A.D., Hayashizaki Y., Ishida J., Jiang P.X., Jones T., Kamiya A., Karlin-Neumann G., Kawai J., Lam B., Lee J.M., Lin J., Liu S.X., Miranda M., Narusaka M., Nguyen M., Onodera C.S., Palm C.J., Pham P.K., Quach H.L., Sakurai T., Satou M., Seki M., Southwick A., Tang C.C., Toriumi M., Yamada K., Yamamura Y., Yu G., Yu G., Shinozaki K., Davis R.W., Theologis A., Ecker J.R.; Submitted (AUG-2001) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                           InterPro; IPR001092; HLH basic. Pfam; PF00010; HLH; 1. SMART; SM00353; HLH; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDLINE=22598051; PubMed=12679534; DOI=10.1093/molbev/msg088; Heim M.A., Jakoby M., Werber M., Martin C., Weisshaar B., Bailey P. "The basic helix-loop-helix transcription factor family in plants: genome-wide study of protein structure and functional diversity."; Mol. Biol. Evol. 20:735-747(2003).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
Town C.D., Kaul S.;
Submitted (JAN-2001)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE FROM N.A.

Lin X., Kaul S., Town C.D., Benito M., Creasy T.H., Haas B.J.

Maiti R., Ronning C.M., Koo H., Fujii C.Y., Utterback T.R.,

Barnstead M.S., Bowman C.L., White O., Nierman W.C., Fraser

Submitted (FEB-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                    Jakoby M.J.,
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[1]
                                                                                                                                                       206
                                                                                                                           107
                                                                                                                                                                                    Similarity 6; Conserv
                                                                                                                                                                                                                                               PS50888; HLH; 1.
259 AA; 28526
                                                                                                                                                         SGSGSG
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 (TrEMBLrel. 16, (TrEMBLrel. 16,
                                               PRELIMINARY;
                                                                                                                                                                                                                                                                                                                                                                                                                                   Heim M.A.,
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the EMBL/GenBank/DDBJ
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 Created)
Last sequence update)
                                                                                                                                                                                   Score 6; DB 2;
Pred. No. 4e+03;
0; Mismatches
                                               PRT;
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                                                                                                                                                                                                                                                                                                                                                                                                    ., Martin C., Weisshaar
//GenBank/DDBJ databases.
helix-loop-helix (bHLH)
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ck T.R.,
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Best Local
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        Submitted (SEP-1999) to the EMBL/GenBan Submitted (SEP-1999) to the EMBL/GenBan EMBL, AJ389668; CAC11057.1; -. GO; GO:0045735; F:nutrient reservoir ac InterPro; IPR003612; AAI.
InterPro; IPR001376; Gliadin.
InterPro; IPR001376; Gliadin.
InterPro; IPR001376; Gliaglutenin.
PFAM; PF000234; Tryp_alpha_amyl; 1.
PRINTS; PR00208; GLIADGUTEN.
PRINTS; PR00209; GLIADGIN.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          EMBL; AJ389674; CAC11087.1; -..
GO; GO:0045735; F:nutrient reservoir ac
InterPro; IPR003612; AAI.
InterPro; IPR003176; Gliadin.
InterPro; IPR001954; Glia-glutenin.
Pfam; PF00234; Tryp_alpha_amyl; 1.
PRINTS; PR00209; GLIADGLUTEN.
PRINTS; PR00209; GLIADIN.
SMART; SM00499; AAI; 1.
                                                                                                                                                                                                                                                                                  Q9FS75;
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2004 (TrEMBLrel. 26,
Gamma-gliadin (Fragment).
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NON_TER
NON_TER
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Spermatophyta; Magnoliophyta; Liliopsida;
Triticeae; Triticum.
                                                                                                                                                                                                                                       Triticum aestivum (Wheat).
Eukaryota; Viridiplantae; Str.
Spermatophyta; Magnoliophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Polymorphisms in two homeologous gamma-gliadin evolution of cultivated wheat."; Genet. Resour. Crop Evol. 0:0-0(0).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            01-MAR-2004 (TrEMBLrel. Gamma-gliadin (Fragment) Name=GAG56D;
                                                                                                                         SEQUENCE FROM N.A.
                                                                                                                                                           "Polymorphisms in two homeologous gamma-gliadin genes evolution of cultivated wheat.";
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                                                                                                                                                                                                                                                                           Name=GAG56D;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                              von Bueren M
                                                                                                                                               Genet. Resour. Crop
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259 AA;
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                                                                                                                                                                                                                                                                                                                                               PRELIMINARY;
 AAI;
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                                                                                                                                               Evol. 0:0-0(0)
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                                                                                                    to the EMBL/GenBank/DDBJ databases.
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26,
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yta; Liliopsida; Poales; Poaceae; Pooidea
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Last
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Pred. No.
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"Insights into the genome evolution of Yersinia pestis through whole genome comparison with Yersinia pseudotuberculosis.";
Proc. Natl. Acad. Sci. U.S.A. 101:13826-13831(2004).

EMBL; BX936398; CAH20373.1; -.

EMBL; BX936398; CAH20373.1; -.

EMBL; BX936398; CAH20825.1; -.

EMBL; BX936398; CAH20825.1; -.

EMBL; BX936398; CAH21048.1; -.

ThterPro; IPR003593; AAA ATPase.

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LipL32 (Fragment)
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Q66FN3;
25-OCT-2004
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SEQUENCE
Leptospira borgpetersenii.
Bacteria; Spirochaetes; Sp
NCBI_TaxID=174;
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                                                                                                                                                                                                                                                                                        ATP-binding.
SEQUENCE 259 AA;
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PubMed=15358858;
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Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
                                         Name=lipL32;
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SEQUENCE
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Plasmid 9.5 kbp pesticin.
Bacteria; Proteobacteria; Gammaproteobacteria; Enterobacteriales;
Enterobacteriaceae; Yersinia.
                                                                                                                                                                                                                                                                                                                                                                                                                                                            05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
25-JUL-2004 (TrEMBLrel. 28, Last annotation update)
ORF11 (ORF 77) (ORFB; putative transposase).
                                                                                                                                                                                                     correlates with pesticin sensitivity in Yersinia pseudotuberculosis.";
J. Bacteriol. 179:2081-2085(1997).
EMBL; AL031866; CAA21334.1; -.
EMBL; AL031866; CAA21402.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 "Molecular evolution and mosaicism of leptospiral outer membrane proteins involves horizontal DNA transfer.";

J. Bacteriol. 186:2818-2828(2004).

EMBL; AY461894; AAS21764.1; -.
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STRAIN=Mus 127;
PubMed=15090524; DOI=10.1128/JB.186.9.2818-2828.2004;
                                                                                               PRINTS; PR00300; CLPPROSMART; SM00382; AAA; 1.
                                                                                                                      InterPro; IPR003593; AAA ATPase.
InterPro; IPR001270; Chaprnin clpA/B.
InterPro; IPR002611; IstB_ATP51nd.
Pfam; PF01695; IstB; 1.
                                                                                                                                                                   EMBL; U59875; AAC44982.1; -.
GO; GO:0005524; F:ATP binding; IEA.
GO; GO:0000166; F:nucleotide binding;
                                                                                                                                                                                                                                                      McDonough K.A., Hare J.M.; monology with a repeated Yersinia pestis DNA sequence IS100
                                                                                                                                                                                                                                                                             STRAIN=EV76-6; PLASMID=9.5 kbp pesticin; MEDLINE=97221614; PubMed=9068660;
                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                             Buchrieser C., Rusniok C., Couve E., Frangeul L., Billav
Kunst F., Carniel E., Glaser P.;
Submitted (OCT-1998) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                  STRAIN=6/69
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                                                                                  ATP-binding; Plasmid
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  186 APRLLI 191
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 27 summaries

Database :

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SUMMARIES

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16	88	34.0	95	μ	ADF09892
17	88	34.0	95	μ	ADJ80271
18	88	34.0	95	_	ADJ80272
19	88	34.0	95	_	ADO07341
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ALIGNMENTS

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                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 88; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Making humanized antibody for converting antibody, by making chimeric antibodies containing complementarity determining region from non-human antibody and appropriate framework sequences of human antibodies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 95 AA;
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                                             447 RFSGSGSGAEFTLTISSLQSEDFAVYYCQQYNNWP 481
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13
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ID ABO27151 standard; protein;
                                                                                                                                                           Query Match
Best Local S
Matches 88
                                                                                                                                                                                                                                                                                                                                                                                                                    comprising making chimeric antibodies containing a complementarity determining region (CDR) from a non-human antibody and appropriate framework sequences (I) of human antibodies. (I) is selected by using canonical CDR structure types of non-human antibody in comparison to germline canonical CDR structure types of human antibody in comparison to germline canonical CDR structure types of human antibodies as the basis for selection, for humanisation. The method is useful for making a humanised antibody or a converted antibody. The method is applicable for converting a subject antibody sequence of any subject species to a less immunogenic form suitable for use in an object species. The method is reliable for identifying suitable human framework sequences to support non-human CDR regions and to provide humanised antibodies that retain high antigen binding with low immunogenicity in humans, without the need for direct comparison of framework sequences, without the need for
                                                                                                                                                                                                                                                                                               determining critically important amino acid residues in the framework, and without the need for multiple iteration and construction to obtain humanised antibodies with suitable therapeutic properties. The antibody has high affinity and low immunogenicity without need for comparing framework sequences between non-human and human antibodies. This sequence represents a human light chain variable region gene segment used in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Making humanized antibody for converting antibody, by making chimeric antibodies containing complementarity determining region from non-human antibody and appropriate framework sequences of human antibodies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human; light chain variable region; VK; humanised antibody;
chimeric antibody; complementarity determining region; CDR;
                                                                                                                                                                                                                                          Sequence 95 AA;
                                                                                                                                                                                                                                                                                  creation of humanised antibodies
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention describes a method of making a humanised antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Example 1; Fig 2; 31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-492151/46.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         12-JUL-2001; 2001US-0305111P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 12-JUL-2002; 2002US-00194975.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            canonical CDR structure type.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human germline light chain variable region gene segment #31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  10-SEP-2003
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Foote J;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (FOOT/) FOOTE J.
                                     447
                                                                                                                                                             88;
                                                                             L
                                                                                                                                                                              Similarity
RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWP 95
                         RFSGSGSGAEFTLTISSLQSEDFAVYYCQQYNNWP 481
                                                                           EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                ELELTQSPATLSVSPGERATLSCRASESVSSDLAWYQQKPGQAPRLLIYGASTRATGVPA 446
                                                                                                                                                           34.0%;
ilarity 92.6%;
Conservative
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                                                                                                                                                           Score 88; DB 1; Length 95; Pred. No. 6.6; 0; Mismatches 7; Indels
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RESULT 3

RESULT 4
ADC99846
ID ADC9
XX
AC ADC9
XC ADC9
XX
DT 01-J
XX
DE Germ

ADC99846 standard; protein;

95

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01-JAN-2004

(first entry)

Germline VK gene L2 region protein SEQ ID

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ADC99850
XX
ADC99XX
AC
ADC9
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AC
ADC9
DT 01-J
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Germ
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Gery
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the germline VK gene region protein of the invention used to analyse the anti-human MUC18 monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to MUC18. The monoclonal antibody of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          anti-human MUC18 monoclonal antibody; heavy; light chain variable domain; cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    invention demonstrates cytostatic activity and may be useful for treal a disease or condition associated with the expression of MUC18 on the cell surface such as tumours, specifically melanoma, oesophageal,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g.
                                                                                                                                                                                                                                                                                                                                                                                             Sequence 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; SEQ ID NO 79; 78pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            tumors, cancers, and other malignancies.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Unidentified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-JAN-2004
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (ABGE-) ABGENIX INC
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                                                             447
                                                                                                                                                                                         387 ELELTQSPATLSVSPGERATLSCRASESVSSDLAWYQQKPGQAPRLLIYGASTRATGVPA 446
61 RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWP 95
                                                                                                                               1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                          88;
                                                                                                                                                                                                                                                                                                Similarity
                                     RFSGSGSGAEFTLTISSLQSEDFAVYYCQQYNNWP 481
                                                                                                                                                                                                                                                                                                                                                                                             AA,
                                                                                                                                                                                                                                                                 Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (first
                                                                                                                                                                                                                                                                                             34.0%;
92.6%;
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                                                                                                                                                                                                                                                              Score 88; DB
Pred. No. 6.6;
0; Mismatches
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RESULT 5
ADC99838
ID ADC99
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XX ADC9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to MUC18. The monoclonal antibody of the invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the cell surface such as tumours, specifically melanoma, oesophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the germline VK gene region protein of the
                                                                                                                   anti-human MUC18 monoclonal antibody; heavy; light chain variable cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour; cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            New human anti-MUC18 monoclonal antibodies, useful for treating a disease or condition associated with expression of MUC18 in a patient, e.g. tumors, cancers, and other malignancies.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    anti-human MUC18 monoclonal antibody; heavy; light chain variable domain;
cytostatic; melanoma; oesophageal; pancreatic; colorectal tumour;
cervical carcinoma; intraepithelial neoplasia; colorectal; breast;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 95
                                                                                                                                                                                                                                             Germline VK
                                                                                                                                                                                                                                                                                                             01-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                 ADC99838 standard; protein; 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          invention used to analyse the anti-human MUCI8 monoclonal antibody
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     invention relates to a novel isolated monoclonal antibody comprising
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                                                                                         cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         387 ELELTQSPATLSVSPGERATLSCRASESVSSDLAWYQQKPGQAPRLLIYGASTRATGVPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            88;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWP 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RFSGSGSGAEFTLTISSLQSEDFAVYYCQQYNNWP 481
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92.6%;
                                                                                             VK region.
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                                                                                                                                                                                   domain;
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Unidentified

(ABGE-) ABGENIX INC

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RESULT
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention demonstrates cytostatic activity and may be useful for treating a disease or condition associated with the expression of MUC18 on the cell surface such as tumours, specifically melanoma, oesophageal, pancreatic or colorectal tumours, carcinomas, particularly cervical carcinomas and cervical intraepithelial neoplasia and cancers including colorectal, breast or lung cancer, as well as other malignancies. The current sequence is that of the gernline VI gene region protein of the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   The invention relates to a novel isolated monoclonal antibody comprising a heavy or light chain amino acid or a heavy or light chain variable domain where the antibody binds to MUC18. The monoclonal antibody of the
                                       28-DEC-2001; 2001US-0346460P
                                                                26-DEC-2002; 2002WO-US041582
                                                                                                                                                                          monoclonal antibody; tumour; MUC18; proliferation; antigen; tumour metastasis; melanoma; metastatic; l
                                                                                                                                                                                                                Anti-MUC18 antibody light chain variable region L2
                                                                                                                                                                                                                                              01-JAN-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New human anti-MUC18 monoclonal antibodies, useful for treating or condition associated with expression of MUC18 in a patient,
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                                                                                                                      WO2003057006-A2
                                                                                                                                                                                                                                                                                                  ADD05454 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         invention used to analyse the anti-human MUC18 monoclonal antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    387
                                                                                                                                                                                                                                                                                                                                                                     61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Similarity
                                                                                                                                                                                                                                                                                                                                                                                 RFSGSGSGAEFTLTISSLQSEDFAVYYCQQYNNWP
                                                                                                                                                                                                                                                                                                                                                                                                                                               ELELTQSPATLSVSPGERATLSCRASESVSSDLAWYQQKPGQAPRLLIYGASTRATGVPA
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                                                                                                                                                                                                                                                                                                                                                                     RESGSGSGTEETLTISSLQSEDFAVYYCQQYNNWP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Conservative
                                                                                                                                                                                                                                             (first
                                                                                                                                                                                                                                                                                                  protein;
                                                                                                                                                                                                                                             entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          34.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        78pp; English.
                                                                                                                                                                                                                                                                                                  95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 88;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             σ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              useful for treating a disease
                                                                                                                                                                                                                                                                                                                                                                                              481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length 95
                                                                                                                                                                          human; light chain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
                                                                                                                                                                                          cytostatic; vaccine;
                                                                                                                                                                                                                  protein,
                                                                                                                                                                                                                     SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 e.g.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       밁
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local S
Matches 88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to a novel monoclonal antibody used for inhibiting tumour growth in an animal. The tumour inhibition process comprises selecting an animal in need of treatment for a tumour, providing a monoclonal antibody comprising a heavy chain amino acid, where the antibody consists of any one of 10 fully defined sequences of 117-123 amino acids given in the specification, and where the monoclonal antibody binds MUC18, and contacting the tumour with the antibody resulting in inhibited proliferation of the cells. The monoclonal antibody has cytostatic and can be used in the production of a vaccine. The monoclonal antibodies against the MUC18 antigen are useful for diagnosing and treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-MUC18 antibody light chain, variable region,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Use of monoclonal antibodies against MUC18 antigen, for diagnosing and treating tumors, inhibiting tumor growth, inhibiting cell invasion associated with melanoma, or increasing survival of an animal having a metastatic tumor.
Use of monoclonal antibodies treating tumors, inhibiting t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       monoclonal antibody; tumour; MUC18; proliferation; cytostatic; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JAN-2004 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 95 AA;
                                                                                     WPI; 2003-577496/54.
                                                                                                                                            Gudas J, Bar-Eli M,
                                                                                                                                                                                                                                                         28-DEC-2001; 2001US-0346460P
                                                                                                                                                                                                                                                                                                                 26-DEC-2002; 2002WO-US041582.
                                                                                                                                                                                                                                                                                                                                                                            17-JUL-2003.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADD05450;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ADD05450 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         protein of the invention.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gudas
                                                                                                                                                                                                    (ABGE-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        387 ELELTQSPATLSVSPGERATLSCRASESVSSDLAWYQQKPGQAPRLLIYGASTRATGVPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 447 RFSGSGSGAEFTLTISSLQSEDFAVYYCQQYNNWP 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          88;
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                                                                                                                                                                                                    ABGENIX INC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibody
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             light chain variable region L2 protein,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  34.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 88; DB Pred. No. 6.6; 0; Mismatches
s against MUC18 tumor growth, :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               DB 1;
6.6;
antigen, f
inhibiting
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       7;
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for diagnosing g cell invasion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  75.
                             and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           60
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RESULT 8
ADF10095
ID TO 95
ID TO 95
ID TO 95
ID TO 12-F
XX ADF1
XX VEGF
XX VEGF
XX VATI
XX WO2C
XX WO2C
XX WO2C
XX O3-h
XX O3-h
PR 01-1
PR 01-1
PR 29-h
XX WPI
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PT Com
PT C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cc tumour growth in an animal. The tumour inhibiting variety used for inhibiting cc selecting an animal in need of treatment for a tumour, providing a cc monoclonal antibody comprising a heavy chain amino acid, where the cantibody consists of any one of 10 fully defined sequences of 117-123 cc amino acids given in the specification, and where the monoclonal antibody binds MUC18, and contacting the tumour with the antibody resulting in cc inhibited proliferation of the cells. The monoclonal antibody has ccytostatic and can be used in the production of a vaccine. The monoclonal antibodies against the MUC18 antigen are useful for diagnosing and ct treating tumours, inhibiting tumour growth (e.g. melanoma, lung tumour or increasing survival of an animal having a metastatic tumour. This sequence represents an anti-MUC18 antibody light chain, variable region, cr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ś
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         밁
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Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      VEGF
                                                                                                                                                Computer optimization of physicochemical properties of comprises analyzing the interactions of amino acids at
                                                                                                                                                                                                                                                                                                   Lazar GA,
                                                                                                                                                                                                                                                                                                                                                                                                                    01-MAR-2002; 2002US-0360843P.
29-MAY-2002; 2002US-0384197P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       03-MAR-2003; 2003WO-US006598
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WO2003074679-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Antibody; stability; solubility; antigen binding affinity; variable region; human; VEGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADF10095
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADF10095 standard; protein; 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    12-SEP-2003
                                                                                                                                                                                                                                                                                                                                                             (XENC-) XENCOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antibody light chain variable region VLk_3-15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      447 RFSGSGSGAEFTLTISSLQSEDFAVYYCQQYNNWP 481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       387 ELELTQSPATLSVSPGERATLSCRASESVSSDLAWYQQKPGQAPRLLIYGASTRATGVPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 88;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA
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                                                                                                                                                                                                                                                                                                   Desjarlais
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                34.0%;
92.6%;
                                                                                                                                                                                                                                                                                                   JR,
                                                                                                                                                                                                                                                                                                   Marshall SA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 0;
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Pred. No. 6.6;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
                                                                                                                                                                                                                                                                                                   Dahiyat
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variable
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Example 6; Fig 16b; 135pp;

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English

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RESULT 9
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAR-2002; 2002US-0360843P
29-MAY-2002; 2002US-0384197P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 95 AA;
                                                                                                                                                                                                                                                                                                                                                                             Computer optimization
                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2003-722066/68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Lazar GA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  03-MAR-2003; 2003WO-US006598
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Antibody light chain variable region VLk_3-15.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADF10197 standard; protein; 95
                                                                                                                                                                                                                                                                                                                                               comprises analyzing the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       variable region; human.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        physico-chemical
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The present invention relates to a method for optimizing at least one physico-chemical property of an antibody by a computational screening method. The method comprises: receiving a template antibody structure; selecting at least one variable position belonging to the antibody structure; selecting at least one amino acid to be considered at the variable position(s); analyzing the interaction of each selected amino acid at each variable position with at least part of the remainder of the antibody, including the selected amino acids at other variable positions;

positions.

Example 16; Fig 40b; 135pp; English

The present invention relates to a method for optimizing at least one physico-chemical property of an antibody by a computational screening method. The method comprises: receiving a template antibody structure; selecting at least one variable position belonging to the antibody variable position(s); analyzing the interaction of each selected amino acid at each variable position with at least part of the remainder of the antibody, including the selected amino acids at other variable positions; and identifying a set of at least one antibody sequence with at least one optimized physico-chemical property. The method is useful for optimizing the physico-chemical properties of an antibody especially the stability, or antigen binding affinity. The optimized antibody may be useful for treating a patient. The present sequence is an antibody variable region sequence used to illustrate the invention.

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29-MAY-2002; 2002US-0384197P
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29-MAY-2002; 2002US-0384197P
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                                                                                                                       variable region
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RESGSGSGTEETLTISSLQSEDEAVYYCQQYNNWP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Desjarlais JR,
                                                                                                                                                                                                                                                                                                                                                                                Ş.
                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                              34.0%;
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                                                                                                                                                                                                                                                 Score 88; DB
Pred. No. 6.6;
0; Mismatches
                                                                                                                                                                                                                                                 0;
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                                                                                                                                                                                                                                                                              6.6;
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                                                                                                                                                                                                                                                                                                            Length 95
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RESULT 13
ADF10096
ID ADF10
RESULT 14
ADF09880
ID ADF09
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Best Local S
Matches 88
                                                                                                                                                                                                                                                                                                   physico-chemical property of an antibody by a computational screening method. The method comprises: receiving a template antibody structure; selecting at least one variable position belonging to the antibody structure; structure; selecting at least one amino acid to be considered at the variable position with at least part of the remainder of the antibody, including the selected amino acids at other variable positions; and identifying a set of at least one antibody sequence with at least one optimized physico-chemical property. The method is useful for optimizing the physico-chemical properties of an antibody, especially the stability, solubility, or antigen binding affinity. The optimized antibody may be useful for treating a patient. The present sequence is an antibody way variable region sequence used to illustrate the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Computer optimization of physicochemical comprises analyzing the interactions of
              ADF09880;
                                                                                                                                                                                                                                                                              Sequence 95 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAR-2002; 2002US-0360843P
29-MAY-2002; 2002US-0384197P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Antibody; stability; solubility; antigen binding affinity; variable region; human; VEGF.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADF10096 standard; protein; 95
                                        ADF09880 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present invention relates to a method for optimizing at least one
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 6; Fig 16b; 135pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2003-722066/68
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   VEGF antibody light chain variable region VLk_3D-15
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (XENC-) XENCOR.
                                                                                                                                        447
                                                                                                                                                                                387 ELELTQSPATLSVSPGERATLSCRASESVSSDLAWYQQKPGQAPRLLIYGASTRATGVPA 446
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                                                                                                                                                                                                                         88; Conservative
                                                                                                                                                                                                                                      Similarity
                                                                                                            RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWP 95
                                                                                                                           RFSGSGSGAEFTLTISSLQSEDFAVYYCQQYNNWP 481
                                                                                                                                                                Desjarlais JR,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                    34.0%;
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                                         95
                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                    Score 88; DB 1; Length 95; Pred. No. 6.6;
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                                                                                                                                                                                                                         Mismatches
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amino acids
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RESULT 15
ADF09888
ID ADF09
XX ADF09
XX ADF09
XX I2-FE
XX ANTi-FE
XX ANTi-FE
XX Cell
KW anti-
XX anti-
XX coll
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention comprises a method for inhibiting cell proliferation associated with expression of MUC18 tumour antigen. The method involves administering anti-MUC18 monoclonal antibody. The method of the invention is useful for inhibiting cell (e.g. melanoma or tumour cell) proliferation associated with the expression of MUC18 tumour antigen, the method is preferably useful for inhibiting tumour metastasis. The method is useful for inhibiting tumour metastasis. The method is useful for inhibiting tumour metastasis tumours, carcinomas, cancer and other malignancies. The present amino acid sequence is used in an alignment with an MUC18 tumour antigen-specific monoclonal antibody of the invention.
                                 Unidentified
                                                               carcinoma; cancer; malignancy.
                                                                              cell proliferation inhibition; MUC18 tumour antigen;
anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
                                                                                                                             Anti-MUC18 monoclonal antibody-related protein #18.
                                                                                                                                                             12-FEB-2004
                                                                                                                                                                                                                           ADF09888 standard; protein; 95 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 95
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MUC18 monoclonal antibody.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Inhibiting cell proliferation associated with expression of MUC18 tumor antigen, involves incubating and inhibiting cell by administering anti-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 2003-598367/56
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        carcinoma; cancer; malignancy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        cell proliferation inhibition; MUC18 tumour antigen;
anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Anti-MUC18 monoclonal antibody-related protein
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                                                                                                                                                                                                                                                                                                                                      447 RFSGSGSGAEFTLTISSLQSEDFAVYYCQQYNNWP 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                       88;
                                                                                                                                                                                                                                                                                                         RFSGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWP
                                                                                                                                                                                                                                                                                                                                                                                                      ELELTQSPATLSVSPGERATLSCRASESVSSDLAWYQQKPGQAPRLLIYGASTRATGVPA
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Pred. No.
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6.6;
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WO2003057837-A2

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ADF09892
ID ADF09892
XX ADF09
XX DF09
XX 12-FE
XX cell
KW cell
KW carci
XX carci
XX Unide
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XX 17-JU
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Best Local S
Matches 88
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                  Gudas J;
                                                                                                                                                                                                                                           cell proliferation inhibition; MUC18 tumour antigen;
anti-MUC18 monoclonal antibody; tumour metastasis inhibition; tumour;
                                                                          28-DEC-2001; 2001US-0346414P
                                                                                                        26-DEC-2002;
                                                                                                                                       17-JUL-2003
                                                                                                                                                                                                 Unidentified
                                                                                                                                                                                                                             carcinoma; cancer; malignancy
                                                                                                                                                                                                                                                                                         Anti-MUC18 monoclonal antibody-related protein #20.
                                                                                                                                                                                                                                                                                                                      12-FEB-2004
                                                                                                                                                                                                                                                                                                                                                                             ADF09892 standard; protein; 95
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                                                (ABGE-) ABGENIX INC
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                                                                                                          2002WO-US041580
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92.6%;
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Pred. No. 6.6;
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The method involves
ethod of the invention
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RESULT 17
ADJ80271
ID 80271
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AC ADJ80
AC
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Matches
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MUC18 mo
                                                                                                                                                                                                          Producing a hybrid antibody or hybrid antibody fragment by operatively linking the selected framework sequences to one or more complementarity determining regions of the initial antibody.
                                                                                                                                                                                                                                                                                                                         WPI; 2003-513753/48.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 03-DEC-2001; 2001US-0336591P
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The invention relates to a method of producing a hybrid antibody or hybrid antibody fragment by: (i) providing an initial antibody having specificity for a target; (ii) determining the sequence of a variable region of the initial antibody; (iii) selecting a first component of the variable region consisting of FR1, FR2, FR3 and FR4; (iv) comparing the

SEQ ID NO 31; 77pp; English.

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RESULT 18
ADJ80272
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                                                                   Producing a hybrid antibody or hybrid antibody fragment linking the selected framework sequences to one or more determining regions of the initial antibody.
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Disclosure; SEQ ID NO 32; 77pp; English
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92.6%;
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The invention relates to a method of producing a hybrid antibody or

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92.6%;
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CC chain. A serine protease triad was not identified in the present cc activity of the procession of the heavy chain.
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Best Local S
Matches 88
                    15-JUL-2004
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                                                          ADO07340;
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                                                                                                                                                                                                                                                                                                                                                                                           Sequence 95
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                                                                                                                                                                                                                                                                           387 ELELTQSPATLSVSPGERATLSCRASESVSSDLAWYQQKPGQAPRLLIYGASTRATGVPA
                                                                                                                                                                                                       447 RFSGSGSGAEFTLTISSLQSEDFAVYYCQQYNNWP 481
                                                                                                                                                                                 61
                                                                                                                                                                                                                                                                                                                       88;
                                                                                                                                                                                                                                                   ۲
                                                                                                                                                                                                                                                                                                                   h 34.0%;
Similarity 92.6%;
88; Conservative
                                                                                                                                                                                 RESGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWP 95
                                                                                                                                                                                                                                                 EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Larrick JW;
                                                                                                                                                                                                                                                                                                                                                                                           AA;
                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3; 92pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /label= CDR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note= "Complementarity determining region 3"
                                                                                                                                                                                                                                                                                                                     Score 88; DB 1; Length 95, Pred. No. 6.6; 0; Mismatches 7; Indels
                                                                                                                                                                                                                                                                                                                       0;
                                                                                                                                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                      446
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Catalytic antibody; human; antibody; gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Human antibody L2 light chain variable region
WPI; 2004-340921/31.
                                  Smider V,
                                                                   (INTE-) INTEGRIGEN INC
                                                                                                   10-OCT-2002; 2002US-0417979P
                                                                                                                                      09-OCT-2003; 2003WO-US032214
                                                                                                                                                                                                          WO2004033658-A2
                                                                                                                                                                                                                                                                            Region
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                                                                                                                                                                                                                                                                                                                                                                                 Region
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Homo sapiens
                                  Larrick JW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                /note= "Complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /note= "Framework region
                                                                                                                                                                                                                                             note= "Complementarity determining region
                                                                                                                                                                                                                                                               label= CDR3
                                                                                                                                                                                                                                                                                              note=
                                                                                                                                                                                                                                                                                                                  'label= FR3
                                                                                                                                                                                                                                                                                                                                                                                                                                                        note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          label=
                                                                                                                                                                                                                                                                                                                                                                                                 label= FR2
note= "Framework region
                                                                                                                                                                                                                                                                                                                                                                    label=
                                                                                                                                                                                                                                                                                              "Framework region
                                                                                                                                                                                                                                                                                                                                                                                                                                                    - CDR1
"Complementarity determining region
                                                                                                                                                                                                                                                                                                                                                                 CDR2
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Novel recombinant catalytic polypeptide useful for cleaving target proteins or for treating or preventing cancers, comprises a human antibody light chain operably joined to a heterologous antibody heavy

Disclosure; Fig 3; 92pp; English

CC recombinant catalytic polypeptides of the invention. These comprise a comprise, and the heavy chain has a serine protease dyad and endopeptidase comprise, and the heavy chain has a predetermined specificity for a comprise the catalytic activity to hydrolyse polypeptides and the comprise the catalytic activity to hydrolyse polypeptides and the construction of a repertoire of proteases with construction attributable to the presence or overexpression comprise and condition attributable to the presence or overexpression company medical condition attributable to the presence or overexpression company medical condition attributable to the presence or overexpression company medical condition attributable to the presence or overexpression company medical condition attributable to the presence or overexpression company medical condition attributable to the presence or overexpression company medical condition attributable to the presence or overexpression company medical protein. The invention also provides mucleic acids considered the catalytic antibodies (which can be used for gene therapy), host cells, transgenic non-human animals, and methods of cleaving a complementary of recombinant catalytic polypeptides by the enzymatic activity of the recombinant catalytic polypeptides by the present of the present of the heavy chain a serior protein the complementarity determining region of the heavy chain a serior protein complementarity determining region of the heavy chain and catalytic polypeptides by the present catalytic complementarity determining region of the heavy chain and catalytic polypeptides by the present catalytic complementarity determining region of the heavy chain and catalytic polypeptides with altering the pres The present sequence is the light chain variable region of human antibody L2. This is one of repertoire of human kappa light chain sequences ADO07310-ADO07349 screened for putative catalytic triads. Several genes encoding such light chains ADO07282-ADO07309 were cloned for use in mutating at least one complementarity determining chain. A serine protease triad was not identified was not identified in the present

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RESULT 21
ADR43440
ID ADR4343
AC ADR43
AC ADR43
XX ADR43
XX DEFRL V
XX ANTIL W
KW DETWN
KW ECZEN
XX UNIde
XX UN
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                                                                                                                           Query Match
Best Local Similarity
                                                                                                   Matches
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                                                                                                                                                                                                                                                  The present invention relates to an antibody comprising a variable light chain region or a variable heavy chain region. The antibody and methods are useful for treating a disorder associated with an abnormally high IgE level, e.g. asthma, altergic rhinitis, eczema, urticaria, atopic dermatitis, or a food allergy. The present sequence represents a FRL which demonstrates improved affinity. This sequence is present in the library of variants in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  New high affinity human monoclonal antibodies, particularly those directed against isotypic determinants of immunoglobulin E, useful for asthma, allergic rhinitis, eczema, urticaria, atopic dermatitis, or a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  antibody; variable light chain; variable heavy chain; Antiallergic; Dermatological; Immunosuppressive; IgE; asthma; allergic rhinitis; eczema; urticaria; atopic dermatitis; food allergy; CDR; FRL.
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                                                                                                                                                                                                          Sequence 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 1; SEQ ID NO 40; 101pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          01-FEB-2003; 2003US-0444229P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     food allergy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 04-NOV-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADR43440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADR43440 standard; peptide; 32 AA
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                                                   443
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   61
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             88;
                                                                                                      30;
  ب
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TANOX INC
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GIPARFSGSGSGTEFTLTISSLQSEDFAVYYC
                          GVPARFSGSGSGAEFTLTISSLQSEDFAVYYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RFSGSGSGAEFTLTISSLQSEDFAVYYCQQYNNWP 481
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Foster C,
                                                                                                                                                                                                       A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ₿
                                                                                                      Conservative
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                                                                                                                           11.6%;
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                                                                                                                           Score 30;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 88; DB 1;
Pred. No. 6.6;
                                                                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Mismatches
                                                                                                                              DB
27;
32
                                                   474
                                                                                                                                                    1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           7;
                                                                                                2
                                                                                                                                                 Length 32;
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                                                                                                   Indels
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                                                                                                   Gaps
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RESULT 22 ADR31585

WO2004070011-A2

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RESULT 23
ADR43442
ID ADR43
XX D4 NC
XX D5 PRL v
XX D6 PRL v
XX D6 PRL v
XX D6 PRL v
XX D7 O1de
XX O1de
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                                                                                                                                                                                                                                                                                                                                                                             Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                The invention relates to a method for generating a humanised high affinity antibody from an antibody of interest. The method involves selecting a suitable human template as the framework for the H (heavy) and L (light) chain variable (V) domains of the high affinity antibody to be made. The method is useful for generating high affinity antibodies useful in diagnostics, prophylaxis and treatment of diseases. The present sequence is murine anti-human IgE antibody (TES-C21) Vk (kappa chain
                                                                   antibody; variable light chain; variable heavy chain; Antiallergic; Dermatological; Immunosuppressive; IgE; asthma; allergic rhinitis; eczema; urticaria; atopic dermatitis; food allergy; CDR; FRL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Generating a humanized, high affinity antibody from an antibody of interest comprises selecting a suitable human template as the framework for the H and L chain variable domains of the high affinity antibody to
                                                                                                                              FRL varaint #13.
                                                                                                                                                           04-NOV-2004
                                                                                                                                                                                                                    ADR43442 standard;
                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 32 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2004-604432/58
                                           Unidentified
                                                                                                                                                                                                                                                                                                                                                                                                                                       variable
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Example 10; SEQ ID NO 40; 100pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Antibody; diagnostic; prophylaxis; therapy; kappa chain variable region; Wk; murine; FR; framework region; mutant; mutein; variant.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               04-NOV-2004
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                                                                                                                                                                                                                                                                                                                                                              Local
                                                                                                                                                                                                                                                                                                        443 GVPARFSGSGSGAEFTLTISSLQSEDFAVYYC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ś
                                                                                                                                                                                                                                                                                                                                               l Similarity
30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TES-C21 antibody (clone 136) FRk3 variant peptide
                                                                                                                                                                                                                                                                                         GIPARFSGSGSGTEFTLTISSLQSEDFAVYYC
                                                                                                                                                                                                                                                                                                                                                                                                                                     region)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Foster C,
                                                                                                                                                                                                                                                                                                                                                  Conservative
                                                                                                                                                         (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                 FR (framework region) variant peptide.
                                                                                                                                                                                                                    peptide;
                                                                                                                                                           entry)
                                                                                                                                                                                                                                                                                                                                                             11.6%;
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                                                                                                                                                                                                                                                                                                                                               0,
                                                                                                                                                                                                                                                                                                                                                              Score 30;
Pred. No.
                                                                                                                                                                                                                    ₽
                                                                                                                                                                                                                                                                                                                                                 Mismatches
                                                                                                                                                                                                                                                                                                                                                                DB 1;
27;
                                                                                                                                                                                                                                                                                                                      474
                                                                                                                                                                                                                                                                                         32
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                                                                                                                                                                                                                                                                                                                                                                             32
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RESULT 24
ADR43441
ID ADR43
XX ADR43
XX ADR43
XX ADR43
XX ADR43
XX DT 04-NC
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Best Local S
Matches 29
                            New high affinity human monoclonal antibodies, particularly those directed against isotypic determinants of immunoglobulin E, useful asthma, allergic rhinitis, eczema, urticaria, atopic dermatitis, food allergy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 antibody; variable light chain; variable heavy chain; Antiallergic; Dermatological; Immunosuppressive; IgE; asthma; allergic rhinitis; eczema; urticaria; atopic dermatitis; food allergy; CDR; FRL.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The present invention relates to an antibody comprising a variable light chain region or a variable heavy chain region. The antibody and methods are useful for treating a disorder associated with an abnormally high IgE level, e.g. asthma, allergic rhinitis, eczema, urticaria, atopic dermatitis, or a food allergy. The present sequence represents a FRL which demonstrates improved affinity. This sequence is present in the library of variants in the specification.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New high affinity human monoclonal antibodies, particularly those directed against isotypic determinants of immunoglobulin E, useful for asthma, allergic rhinitis, eczema, urticaria, atopic dermatitis, or a food allergy.
                                                                                                                                                                     WPI; 2004-604433/58.
                                                                                                                                                                                                                         Singh S,
                                                                                                                                                                                                                                                                                                                                       01-FEB-2003; 2003US-0444229P
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                                                                                                                                                                                                                      Foster C,
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ilarity 90.6%;
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Matches 29
                                                    The invention relates to a method for generating a humanised high affinity antibody from an antibody of interest. The method involves selecting a suitable human template as the framework for the H (heavy) and L (light) chain variable (V) domains of the high affinity antibody to be made. The method is useful for generating high affixity antibodies useful in diagnostics, prophylaxis and transment of diseases. The present sequence is murine anti-human IgE antibody (TES-C21) Vk (Kappa chain variable region) FR (framework region) variant peptide.
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Synthetic.
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                                                                                                                                                                                                                                                                                                                                                                                                                 Generating a humanized, high affinity antibody from an antibody of interest comprises selecting a suitable human template as the frame for the H and L chain variable domains of the high affinity antiboo
                                                                                                                                                                                                                                                                                                                                 Example 10;
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e; FR; framework region; mutant; mutein; variant.
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RESULT 27
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Cytostatic; antidiabetic; neuroprotective; cerebroprotective;
                                                       18-JUN-2002
                                                                                                                                                                                                                                                                                                  Sequence 32 AA;
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                          Insulin/insulin-like growth factor receptor-binding peptide #2850.
                                                                                                              AAU90894 standard;
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                                                                                                                                                                     The invention relates to a method of modulating insulin activity in mammalian cells by administering a peptide that binds the insulin receptor (IR). A composition containing a peptide, optionally expressed from gene therapy vectors, that binds to Site 1 of IR and an insulin agonist are useful for treating diabetes. Also, peptides that are antagonists of the insulin-like growth factor (IGF-1) receptor are useful for treating insulin-like growth factor (IGF)-sensitive tumours (e.g. of prostate and breast) and diabetic retinopathy, while IGF-1 receptor agonists are useful for treating neurological diseases, including stroke and diabetic neuropathy. The peptides are also useful in screening for compounds that bind to IR or IGF-1 receptor, potential therapeutics and research reagents. AAU88034-AAU90957 represent IR and/or IGF-1 receptor-binding peptides and related amino acid sequences of the
                                                                                                                                                                                                                                                                                                                                                                                                                                       Modulating insulin activity in mammalian cells, for treating e.g. diabetes and tumors, comprises using peptides that bind to insulin insulin-like growth factor receptors.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Beasley J, Blume AJ,
Brissette R, Spetzle:
Hansen PH, Ravera M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ophthalmological; insulin; receptor; gene therapy; diabetes; insulin-like growth factor-1; IGF-1; tumour; prostate; breast; diabetic retinopathy; neurological diseases; stroke; diabetic
                                                                                                                           Sequence 26
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, Spetzler J, Cheng W,
Ravera M, Hsiao K;
                                                                Conservative
                                                                            9.3%;
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                                                                             Score 24;
Pred. No.
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Ostergaard (
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Result
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                PCT-US91-02942-67
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
                                                                                                                                                                                                                                                           Sequence 67, Application PC/TUS9102942
GENERAL INFORMATION:
APPLICANT: ROTHLEIN, ROBERT
APPLICANT: ADAIR, JOHN R
APPLICANT: ATHWAL, DILJEET S
TITLE OF INVENTION: HUMANIZED CDR-GRAFTED ICAM-1 ANTIBODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              No.
                                                                                                                               STREET: 1225
STREET: Washington
CITY: Washington
STATE: D.C.
TTCA
                             COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
                                                                                                                                                                                                                            CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                NUMBER OF SEQUENCES:
                                                                                                              COUNTRY: U
ZIP: 20036
                                                                                                                                                                                                          ADDRESSEE:
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seq length: 2000000000
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Match
                                                                                                                                                                                     E: Sterne, Kessler, Goldstein & Fox 1225 Connecticut Ave. NW Suite 300
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Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2005 Compus
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US-08-207-169A-7
US-08-331-398A-54
US-08-331-397B-54
US-08-463-163-5
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                   Version #1.25
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Sequence 54, Appl
Sequence 5, Appli
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Sequence 7, Appli
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APPLICATION NUMBER:

PCT/US91/02942

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-08-207-169A-7
             TELEPHONE: (703) 413-3000
TELEPAX: (703) 413-2220
TELEFAX: (24855 OPAT UR
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 18 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 7 Patent No.
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Best Local Similarity
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
COMPUTER: Patent In Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/207,169A
FILING DATE: 08-MAR-1994
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (202) 833-8716
INFORMATION FOR SEQ ID NO: (
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: GRANDI, GUIDO
APPLICANT: DE FERRA, FRANCI
APPLICANT: TOSI, CLAUDIO
APPLICANT: TORTORA, ORNELL
APPLICANT: CUZZONI, ANNA
TITLE OF INVENTION: RECOMB:
TITLE OF INVENTION: EXCEL:
TITLE OF INVENTION: BACILLI
NUMBER OF SEQUENCES: 16
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CLASSIFICATION: 435
CLASSIFICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: GB 900
FILING DATE: 27-APR-1990
ATTORNEY (AGENT INFORMATION:
POWER: POW TAME:
ANAME: POW TAME:
                                                                                                                                        ATTORNEY AGENT INFORMATION:
NAME: Oblon, No. 5674712man F.
REGISTRATION NUMBER: 24,618
REFERENCE/DOCKET NUMBER: 2564-
TELECOMMUNICATION INFORMATION:
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TELECOMMUNICATION INFORMATION:
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ADDRESSEE:
STREET: 175
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ZIP: 22202
                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE: Virginia
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Arlington
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TOPOLOGY:
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1755 S. Jefferson Davis Highway, Suite 400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TORTORA, ORNELLA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GRANDI, GUIDO
DE FERRA, FRANCESCA
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                                                                                                                            (703) 413-3000
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MEDIUM TYPE: Floppy disk
COMPUTER: LBM PC comparable
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PACENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/331,398A
FILING DATE: 28-OCT-1994
CLASSIFICATION ATA:
APPLICATION NUMBER: US 07/767,331
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/596,289
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
NAME: Hunter, Tom
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Patent No. 5608
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Best Local Similarity
                                                                                                                                       Matches
                                                                                                                                                                                                    Query Match
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                                                                                                                                                                                                                                                                                                                                                                                                                                        TELEPHONE: (415) 543-9600
TELEFAX: (415) 543-5043
INFORMATION FOR SEQ ID NO: 54
SEQUENCE CHARACTERISTICS:
LENGTH: 16 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                             STRANDEDNESS:
TOPOLOGY: linear
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES: 68
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Plaza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 01
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Single Chain B3 Antibody Fusion Proteins TITLE OF INVENTION: and Their Uses (as amended)
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TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: One ....
CITY: San Francisco
                                                                                                                                Y Match 6.2%; So Local Similarity 100.0%; loca
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Hunter, Tom
REGISTRATION NUMBER: 38,498
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY: USA
                                                                371 seeeeseeseeses 386
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              369 VTSGGGGSGGGGGGGS 386
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FitzGerald, David
Brinkmann, Ulrich
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Conservative
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internal
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Pred. No.
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US-08-331-397B-54
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APPLICANT: Pastan, Itai
APPLICANT: Benhar, Itai
TITLE OF INVENTION: Chime
TITLE OF INVENTION: Speci
TITLE OF INVENTION: There
                                                                                                                                                                                                                         Sequence 5, Application US/08463163 Patent No. 5696237
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTION DATA:
APPLICATION NATA:
APPLICATION NATA:
CLASSIFICATION 28-OCT-1994
CLASSIFICATION 28-OCT-1994
CLASSIFICATION 25-OCT-1994
CLASSIFICATION DATA:
APPLICATION UMBER: US 07/767,331
FRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/767,331
FILING DATE: 30-SEP-1991
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                                                                                                                                                                                                          GENERAL INFORMATION:
                                                      APPLICANT: Waldmann, Thomas A.
APPLICANT: Queen, Cary L.
TITLE OF INVENTION: Recombinant Antibody-Toxin Fusion Protein
NUMBER OF SEQUENCES: 12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 0
FILING DATE: 12-OCT-1990
ATTORNEY/AGENT INFORMATION:
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew
STREET: One Market Plaza, Steuart Street Tower
                                                                                                                                              APPLICANT:
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STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
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REFERENCE/DOCKET NUMBER: 01
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One Market Plaza, Steuart Street Plaza
                                                                                                                                         FitzGerald, David J
Chaudhary, Vijay K.
Pastan, Ira H.
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Specific Antibody Fragments, Fusion Proteins, and Uses
Thereof
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CITY: San Francisco
STATE: California
COUNTRY: USA
COUNTRY: USA
COUNTRY: USA
CONCUTTER READALE PORM:
NEDIUM TYPE: Floppy disk
COMPUTER TYPE: Floppy disk
COMPUTER: ISA
CONCUTTER SPECIAL RESET ON
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US 06/227,227
FILING DATE: 2-JAN-1985
CLASSIFICATION DATA:
APPLICATION NUMBER: US 06/211,227
FILING DATE: 2-JAN-1981
PRIOR APPLICATION NUMBER: US 07/341,361
FRIOR APPLICATION NUMBER: US 07/341,361
FRIUNG DATE: 21-AER-1989
PRIOR APPLICATION NUMBER: US 07/341,361
FILING DATE: 21-AER-1989
PRIOR APPLICATION NUMBER: US 07/341,361
FILING DATE: 10-AER-1989
PRIOR APPLICATION NUMBER: US 07/341,361
FILING DATE: 10-AER-1989
PRIOR APPLICATION NUMBER: US 07/341,361
FILING DATE: 10-AER-1989
PRIOR APPLICATION NUMBER: US 07/341,361
FILING DATE: 10-AER-1987
FILING DA
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Title:

Run on:

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US-10-194-975-84
; Sequence 84, Application US/10194975
; Publication No. US20030039649A1
; GENERAL INFORMATION:
; APPLICANT: FOOTE, Jefferson
; TITLE OF INVENTION: Super Humanized Antibodies
; FILE REFERENCE: 501231.01
; CURRENT APPLICATION NUMBER: US/10/194,975
; CURRENT APPLICATION NUMBER: US 60/305,111
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seq length: 2000000000
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Match
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Gapop 10.0 , Gapext 0.5
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259
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Listing first 17 summaries
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                                                                                                                                                                                                                         GenCore version 5.1.6 (c) 1993 - 2005 Compugen Ltd.
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US-10-194-975-85
US-10-308-817-32
US-10-308-817-31
US-10-453-698-31
US-10-453-698-32
US-10-379-392-95
US-10-379-392-96
US-10-984-960A-106
US-10-923-068-75
US-10-923-068-75
US-10-984-960A-70
US-10-984-960A-70
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US-10-901-736-41
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Sequence 31, R
Sequence 31, R
Sequence 32, R
Sequence 32, R
Sequence 95, R
Sequence 95, R
Sequence 96, R
Sequence 97, R
Sequence 106, R
Sequence 175, R
Sequence 175, R
Sequence 175, R
Sequence 34, R
Sequence 34, R
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Result No.

Score

RESULT 1

Database

Maximum Minimum

80 80

Searched:

Scoring table: Sequence: Perfect score:

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; PRIOR FILING DATE: 2001-07-12; NUMBER OF SEQ ID NOS: 122; SOFTWARE: PatentIn version 3.1; SEQ ID NO 84; LENGTH: 95; TYPE: PRT; ORGANISM: Homo sapiens US-10-194-975-84
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/10/194,975
CURRENT FILING DATE: 2002-10-10
PRIOR APPLICATION NUMBER: US 60/305,111
PRIOR FILING DATE: 2001-07-12
NUMBER OF SEQ ID NOS: 122
SOFTWARE: Patentin version 3.1
SEQ ID NO 85
LENGTH: 95
; TYPE: PRT ; ORGANISM: human US-10-308-817-31
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                                                                  NUMBER OF SEQ ID NOS: 195
SOFTWARE: PatentIn version
SEQ ID NO 31
                                                                                                                                                                     Sequence 31, Application US/10308817 publication No. US20030219861A1 GENERAL INFORMATION:
APPLICANT: Rother, Russell APPLICANT: Wu, Dayang TITLE OF INVENTION: HYBRID ANTIBODIES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local (
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Best Local Similarity
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                                                                                                                 FILE REFERENCE: 1087-37
CURRENT APPLICATION NUMBER: US/10/308,817
CURRENT FILING DATE: 2002-12-03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Foote, Jefferson TITLE OF INVENTION: Super Humanized Antibodies FILE REFERENCE: 501231.01
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Homo sapiens
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                                                  LENGTH: 95
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                                                                                                                                                                        ; ORGANISM: human US-10-453-698-31
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US-10-453-698-31
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                                                                                                                                                                                                                                                                                          Sequence 31, Application US/10453698
Publication US/20040038308A1
GENERAL INFORMATION:
APPLICANT: Rother, Russell
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 82 CIP (1087-37 CIP)
CURRENT APPLICATION NUMBER: US/10/453,698
CURRENT FILING DATE: 2003-06-03
                                                                                                       Matches
                                                                                                                                                                                                                          SEQ ID NO 31
LENGTH: 95
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LENGTH: 95
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Publication No. US20030219861A1
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Best Local Similarity
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APPLICANT: Wu, Dayang
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 1087-37
CURRENT APPLICATION NUMBER: US/10/308,817
CURRENT FILING DATE: 2002-12-03
NUMBER OF SEQ ID NOS: 195
SOFTWARE: PatentIn version 3.1
                                                                                                                                                                                                                                                          CURRENT FILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 196
SOFTWARE: PatentIn version 3.2
                                                                                                                    Local Similarity
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                                                     387 ELELTQSPATLSVSPGERATLSCRASESVSSDLAWYQQKPGQAPRLLIYGASTRATGVPA
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RFSGSGSGAEFTLTISSLQSEDFAVYYCQQYNNWP 481
                                EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRLLIYGASTRATGIPA
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92.6%;
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Pred. No. 3;
0; Mismatches
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Pred. No. 3;
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Sequence 32, Application US/10453698
Publication No. US20040038308A1
GENERAL INFORMATION:
APPLICANT: Rother, Russell
TITLE OF INVENTION: HYBRID ANTIBODIES
FILE REFERENCE: 82 CIP (1087-37 CIP)
CURRENT APPLICATION UMBER: US/10/453,698
CURRENT FILING DATE: 2003-06-03
NUMBER OF SEQ ID NOS: 196
SOFTWARE: Patentin version 3.2
SEQ ID NO 32
LENGTH: 95
                                                                                                                                                                                                             ; SOFTWARE: PatentIn version 3.2
; SEQ ID NO 95
; LENGTH: 95
; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-379-392-95
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US-10-453-698-32
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Best Local Similarity
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Best Local Similarity
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APPLICANT: Desjarlais, John Rudolf
APPLICANT: Marshall, Shannon Alicia
APPLICANT: Dahiyat, Bassil I.
TITLE OF INVENTION: ANTIBODY OPTIMIZATION
FILE REFERENCE: A-71386-3 463077-236
                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/379,392
CURRENT FILING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/360,843
                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2002-0
NUMBER OF SEQ ID NOS: 184
                                                                                                                                                                                                                                                                                                                                                           PRIOR FILING DATE: 2002-03-01 PRIOR APPLICATION NUMBER: US 60/384,197
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ORGANISM: human
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                  447 RFSGSGSAEFTLTISSLQSEDFAVYYCQQYNNWP 481
                                                                                       387 ELELTQSPATLSVSPGERATLSCRASESVSSDLAWYQQKPGQAPRLLIYGASTRATGVPA 446
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61 RESGSGSGTEFTLTISSLQSEDFAVYYCQQYNNWP
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US-10-379-392-96

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APPLICANT: Zhang, Dongxiao
TITLE OF INVENTION: METHODS OF SCREENING FOR MONOCLONAL
TITLE OF INVENTION: METHODIES WITH DESIRABLE ACTIVITY
FILE REFERENCE: EPIT-007
CURRENT APPLICATION NUMBER: US/10/869,355
CURRENT FILING DATE: 2004-06-15
PRIOR APPLICATION NUMBER: 60/483,391
PRIOR APPLICATION NUMBER: 60/484,185
PRIOR APPLICATION NUMBER: 60/484,185
PRIOR FILING DATE: 2003-06-26
PRIOR FILING DATE: 2003-06-36
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APPLICANT: Dahiyat, Bassil I.
TITLE OF INVENTION: ANTIBODY OPTIMIZATION
PILE REFERENCE: A-71386-3 463077-236
CURRENT APPLICATION NUMBER: US/10/379,392
CURRENT FILLING DATE: 2003-03-03
PRIOR APPLICATION NUMBER: US 60/360,843
PRIOR APPLICATION NUMBER: US 60/384,197
PRIOR FILLING DATE: 2002-03-01
PRIOR PILLING DATE: 2002-05-29
NUMBER OF SEQ ID NOS: 184
                                                                                                                                                                                                                          ; ORGANISM: Oryctolagus cuniculus US-10-869-355-22
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                                                                                                                                                                                                                                                                         SOFTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 22
LENGTH: 95
TYPE: PRT
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Best Local Similarity 92.6%;
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Best Local Similarity 92.6%;
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LENGTH: 95
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Publication No. US20040110226A1
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RFSGSGSGAEFTLTISSLQSEDFAVYYCQQYNNWP 481
                                                     Application US/10869355
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Desjarlais, John Rudolf
                                                                                                                                            Conservative
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                                                                                                                                        0; Mismatches
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Pred. No. 3;
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US-10-923-068-84

Sequence 84, Application US/10923068 Publication No. US20050042664A1 GENERAL INFORMATION:

APPLICANT: Wu, Herren

RESULT 12

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                                                                                                                                                        ; ORGANISM: Homo sapiens US-10-923-068-75
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VS-10-984-960A-106
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APPLICANT: Gallo, Michael

APPLICANT: Chui, Daniel

APPLICANT: Zhong, Haibong

APPLICANT: Larochelle, William J.

APPLICANT: Larochelle, William J.

APPLICANT: Larochelle, William J.

APPLICANT: LOROCHELLE, WILLIAM J.

APPLICANT: LOROCHELLE, WILLIAM J.

APPLICANT: LOROCHELLE, WILLIAM J.

APPLICANTON: ANTHONOMICS AGAINST SECRETORYLEUKOCYTE PROTEASE INHIBITOR

FILE REFERENCE: Cura 970

CURRENT FILING DATE: 2004-11-08

PRIOR APPLICATION NUMBER: 60/518,275

PRIOR FILING DATE: 2003-11-07
                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 75, Application US/10923068 Publication No. US20050042664A1 GENERAL INFORMATION:
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SOPTWARE: CuraSeqList version 0.1
SEQ ID NO 106
LENGTH: 95
TYPE: PRT
ORGANISM: Homo sapiens
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                                                                                                                                                                                                               SEQ ID NO 75
LENGTH: 32
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Best Local Similarity 92.6%;
                                                                                                Best
                                                                                                                   Query Match
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                                                                                                                                                                                                                                                                                                                                   APPLICANT: Wu, Herren
APPLICANT: Dall'Acqua, William
APPLICANT: Damschroder, Melissa
TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES
FILE REFERENCE: AE600US
                                                                                                                                                                                                                                                      NUMBER OF SEQ ID NOS: 518
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/923,068
CURRENT FILING DATE: 2004-08-20
                                                                                                                                                                                               TYPE: PRT
                                                                                            Local
                      443 GVPARFSGSGSGAEFTLTISSLQSEDFAVYYC 474
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                                                                          Similarity
30; Conserv
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GIPARFSGSGSGTEFTLTISSLQSEDFAVYYC
                                                                            Conservative
                                                                                            11.6%;
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Pred. No.
                                                                                          Score 30;
Pred. No.
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                                                                          Mismatches
                                                                                                                   DB 1;
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                                                                                                                 Length 32;
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                                                                                                                                                                                                                                                                                                         US-10-984-960A-70
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US-10-984-960A-34
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 84
LENGTH: 32
                                                                                                                                                                                                                                          Sequence 70, Application US/10984960A Publication No. US20050142137A1 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: CuraSeqList version 0.1
SEQ ID NO 34
LENGTH: 32
TYPE: PRT
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Best Local Similarity
APPLICANT: Gallo, Michael
APPLICANT: Chui, Daniel
APPLICANT: Zhong, Haihong
APPLICANT: Zhong, Haihong
APPLICANT: Ara, Gulshan
TITLE OF INVENTION: AMTIBODIES AGAINST SECRETORYLEUKOCYTE PROTEASE INHIBITOR
FILE REFERENCE: Cura 970
CURRENT APPLICATION NUMBER: US/10/984,960A
CURRENT FILING DATE: 2004-11-08
PRIOR APPLICATION NUMBER: 60/518,275
PRIOR APPLICATION NUMBER: 60/518,275
PRIOR FILING DATE: 2003-11-07
NUMBER OF SEQ ID NOS: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILE REFERENCE: Cura 970
CURRENT APPLICATION NUMBER: US/10/984,960A
CURRENT FILING DATE: 2004-11-08
PRIOR APPLICATION NUMBER: 60/518,275
PRIOR FILING DATE: 2003-11-07
NUMBER OF SEQ ID NOS: 112
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Gallo, Michael
APPLICANT: Chui, Daniel
APPLICANT: Zhong, Haihong
APPLICANT: Ara, Gulshan
APPLICANT: LaRochelle, William J.
TITLE OF INVENTION: ANTIBODIES AGAINST SECRETORYLEUKOCYTE PROTEASE INHIBITOR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION NUMBER: US/10/923,068
CURRENT FILING DATE: 2004-08-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Dall'Acqua, William APPLICANT: Dammethroder, Melissa TITLE OF INVENTION: HUMANIZATION OF ANTIBODIES FILE REFERENCE: AE600US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Local
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93.8%;
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Pred. No. 16;
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Pred. No. 16;
0; Mismatches
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; Sequence 41, Application US/10901736
; Publication No. US20050169909A1
; GENERAL INFORMATION:
; APPLICANT: TANOX, INC.
APPLICANT: SINGH, Sanjaya
; APPLICANT: FUNGH, Sanjaya
; APPLICANT: FUNGG, Sek Chung
; TITLE OF INVENTION: Identification of Unique, Hi
; FILE REFERENCE: TNX-1030
; CURRENT APPLICATION NUMBER: US/10/901,736
; CURRENT APPLICATION 2004-07-29
; CURRENT APPLICATION SIMPLE CONTROL OF THE COURTENT SITEMAN CONTROL OF THE COURTE CO
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APPLICANT: SINGH, Sanjaya

APPLICANT: HUANG, Danyang

APPLICANT: HUANG, Danyang

APPLICANT: HUANG, Danyang

APPLICANT: HUANG, Danyang

APPLICANT: PUNG, Sek Chung

CURRENT APPLICATION IDER: US/10/901,736

CURRENT APPLICATION NUMBER: US/10/901,736

CURRENT FILING DATE: 2004-07-29

PRIOR APPLICATION NUMBER: 60/444,229

PRIOR APPLICATION NUMBER: PCT/US04/02892

PRIOR FILING DATE: 2004-02-02

PRIOR FILING DATE: 2004-02-02
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SOFTWARE: PatentIn version 3.2
SEQ ID NO 40
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Publication No.
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Best Local Similarity
Matches 30; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match
Best Local
PRIOR APPLICATION NUMBER: 60/444,229
PRIOR FILING DATE: 2003-02-01
PRIOR APPLICATION NUMBER: PCT/US04/02892
PRIOR FILING DATE: 2004-02-02
PRIOR APPLICATION NUMBER: PCT/US04/02894
PRIOR FILING DATE: 2004-02-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: ARTIFICIAL
FEATURE:
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TYPE: PRT
ORGANISM: Homo sapiens
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Pred. No.
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Sequence 42, Application US/10901736

Publication No. US20050169909A1

GENERAL INFORMATION:

APPLICANT: TANOX, INC.
APPLICANT: SINGH, Sanjaya
APPLICANT: HUANG, Danyang
APPLICANT: HUANG, Danyang
APPLICANT: HUANG, Danyang
APPLICANT: HUANG, Danyang
APPLICANT: HUANG, Sek Chung
ITITLE OF INVENTION: Identification of Unique, High Affinity IgE Epitopes
FILE REFERENCE: TWX-1030

CURRENT FILING DATE: 2004-07-29
PRIOR APPLICATION NUMBER: 60/444,229
PRIOR APPLICATION NUMBER: 60/444,229
PRIOR PILING DATE: 2003-02-01
PRIOR APPLICATION NUMBER: PCT/US04/02892
PRIOR APPLICATION NUMBER: PCT/US04/02892
PRIOR PILING DATE: 2004-02-02
PRIOR PILING DATE: 2004-02-02
INUMBER OF SEQ ID NOS: 77
SOFTMARE: PatentIn version 3.2
LENGTH: 32
TYPE: PRT
ORGANISM: ARTIFICIAL
FEATURE:
OTHER INFORMATION: FRL3 VARIANT 13
US-10-901-736-42
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SOFTWARE: PATENTIN VERSION 3.2
SEQ ID NO 41
LENGTH: 32
TYPE: PRT
ORGANISM: ARTIFICIAL
FEATURE:
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Search completed: September 28, 2005, 10:33:18 Job time: 0.001 secs
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US-10-901-736-42
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                                                                                                                                                                   Query Match 11.2%; Score 29; DB 1; Best Local Similarity 90.6%; Pred. No. 16; Matches 29; Conservative 0; Mismatches
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Best Local Similarity 90.6%;
Matches 29; Conservative
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A,Status: preliminary
A,Molecule type: DNA
A,Molecule type: DNA
A,Residues: 1-84 <WAG>
A,Cross-references: UNIPROT:Q9UL83; EMBL:X67183
C,Superfamily: immunoglobulin V region; immunoglobulin homology
C,Keywords: heterotetramer; immunoglobulin
F;5-79/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                        Ig kappa chain V region - human (Species: Homo sapiens (man) (C; Species: Homo sapiens (man) (C; Date: 13-Jan-1995 #sequence_revision 13-Jan-1995 #text_change 09-Jul-2004 (C; Accession: S34099 R; Wagner, S.D.; Luzzatto, L. Eur. J. Immunol. 23, 391-397, 1993 Eur. J. Immunol. 23, 391-397, 1993 A; Title: V-kappa gene segments rearranged in chronic lymphocytic leukemia are distribute A; Reference number: S34076; MUID:93170387; PMID:8436174 A; Accession: S34099
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Maximum Match 100%
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                                                                                    Query Match 30.9%;
Best Local Similarity 95.2%;
Matches 80; Conservative
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SVSPGERATLSCRASQSVSSNLAWYQQKPGQAPRILIYGASTRATGIPARFSGSGSGTEF 60
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259
1 QVQLLESGAEVKKP
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Match Length DB
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                                                                                    Score 80; DB 1;
Pred. No. 0;
0; Mismatches
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                                                                                      4.
                                                                                                                               Length 84;
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                                                                                    Gaps
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Search completed: September 28, 2005, 10:42:59 Job time : 0.001 secs

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Result
No.
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       Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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DB seq length: 2000000000
     Score
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Match
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1440
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1: /cgn2_6/ptodata/1/ina/5A_COMB.seq:*

2: /cgn2_6/ptodata/1/ina/5B_COMB.seq:*

3: /cgn2_6/ptodata/1/ina/6A_COMB.seq:*

4: /cgn2_6/ptodata/1/ina/6B_COMB.seq:*

5: /cgn2_6/ptodata/1/ina/PCTUS_COMB.seq:*

6: /cgn2_6/ptodata/1/ina/backfiles1.seq:*
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      atgaaccggggagtcccttt.....
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     1213
1415
1421
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US-08-394-388A-2
US-08-394-388A-3
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Patent No. 523418
Sequence 4, Appli
Sequence 3, Appli
Sequence 7, Appli
Sequence 1013, Appli
Sequence 1013, Appli
Sequence 28, Appl
Sequence 28, Appli
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5223418-1

LENGTH: 1213

APPLICATION NUMBER: US/-FILING DATE: 28-SEP-1990 (SEQ ID NO:1:

US/07/589,979

622.8 43.2 1742 3 US-08-466-368-3 43.2 1742 4 US-08-470-998-1 622.8 43.2 1742 4 US-08-328-500-8 622.8 43.2 2589 4 US-08-472-988A-5 621.2 43.1 1273 4 US-08-236-368-1 621.2 43.1 1416 1 US-08-236-311-2 621.2 43.1 1416 1 US-08-236-311-2 621.2 43.1 1416 3 US-08-457-918-2 621.2 43.1 1416 3 US-08-457-918-2 621.2 43.1 1416 2 US-08-457-918-2 621.2 43.1 3426 2 US-08-418-848A-3 621.2 43.1 3426 2 US-08-418-848A-3 621.2 43.1 3426 2 US-08-418-848A-6 621.2 43.1 3426 2 US-08-418-848A-6 621.2 43.1 3721 2 US-08-418-848A-6 621.2 43.1 3721 2 US-08-418-848A-6 621.2 43.1 3993 2 US-08-418-848A-7 621.2 43.1 4059 2 US-08-418-848A-7 621.2 43.1 4059 2 US-08-418-848A-7 621.2 43.1 4632 2 US-08-418-848A-8 619.6 43.0 1009 6 S223394-8	18 43.2 1742 3 US-08-466-368-3 Sequence 18 43.2 1742 4 US-08-470-998-1 Sequence 18 43.2 1742 4 US-08-328-500-8 Sequence 18 43.2 1742 4 US-08-328-500-8 Sequence 18 43.2 2589 4 US-08-472-888A-5 Sequence 18 43.2 2589 4 US-08-472-888A-5 Sequence 18 43.1 1273 3 US-08-466-368-1 Sequence 19 43.1 1273 3 US-08-328-500-1 Sequence 19 43.1 1416 1 US-08-236-311-2 Sequence 19 43.1 1416 3 US-08-457-918-2 Sequence 19 43.1 1416 3 US-08-457-918-2 Sequence 19 43.1 1416 3 US-08-418-848A-3 Sequence 10 43.1 3426 2 US-08-418-848A-4 Sequence 10 43.1 3721 2 US-08-418-848A-6 Sequence 10 43.1 3933 2 US-08-418-848A-6 Sequence 11 43.1 4632 2 US-08-418-848A-6 Sequence 12 43.1 4632 2 US-08-418-848A-6 Sequence 13 43.1 4632 2 US-08-418-848A-8 Sequence 14 43.0 1009 6 5223394-8 Patent No.	45	44	43	42	41	40	39	8	37	36	35	34	ü	32	31	30	29	
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ALIGNMENTS

RESULT 1

F223418-1

;Patent No. 5223418
; Patent No. 5223418
; APPLICANT: ARCURI, EDWARD J.;BRAWNER, MARY E.;DONOVAN
; J.;GERBER, ROBERT G.;KELLER, JOHN A.
; TITLE OF INVENTION: METHOD OF IMPROVING THE YIELD OF
;HETEROLOGOUS PROTEINS PRODUCED BY STREPTOMYCES LIVIDANS
; NUMBER OF SEQUENCES: 2
; CURRENT APPLICATION DATA:
; CURRENT APPLICATION DATA:

EDWARD J.; BRAWNER, MARY E.; DONOVAN,

Вb	δλ	Ъ	8	В	89	Db	Qy	₽	Q	Ъ	Ş	д	Qy	Db	Ş	Best Lo Matches	М,
499 CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT 558	421 CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT 480	439 CTAGTGTTCGGATTGACTGCCAACTCTGACACCCACCTGCTTCAGGGGCAGAGCCTGACC 498	361 CTAGTGTTCGGATTGACTGCCAACTCTGACACCCCACCTGCTTCAGGGGCAGAGCCTGACC 420	379 ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGAGGTGCAATTG 438	301 ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAAGGACCAGAAGGAGGAGGAGGAGGTGCAATTG 360	319 GACTCAAGAAGAAGCCTTTGGGACCAAGGAAACTTCCCCCTGATCATCAAGAATCTTAAG 378	241 GACTCAAGAAGACCTTTGGGACCAAGGAAACTTCCCCCCTGATCATCAAGAATCTTAAG 300	259 ATTCTGGGAAATCAGGGCTCCTTCTTAACTAAAGGTCCATCCA	181 ATTCTGGGAAATCAGGGCTCCTTCTTAACTAAAGGTCCAATCCAAGCTGAATGATCGCGCT 240	199 TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCAACCAGATAAAG 258	121 TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCCAACCAGATAAAG 180	139 GCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAAAAAAGGGGATACAGTGGAACTGACC 198	61 GCAGCCACTCAGGGAAAGAAAGTGGTGGTGCTGGGCAAAAAAAGGGGGATACAGTGGAACTGACC 120	79 ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCCAACTGGCGCTCCTCCCA 138	1 ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA 60	Local Similarity 97.7%; Pred. No. 3.8e-138; Endels 0; Gaps 0; es 634; Conservative 0; Mismatches 15; Indels 0; Gaps 0;	43.4%; Score 625; DB

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                                                      PCT-US92-08090-4
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TELEPAX: 404-572-6555
INFORMATION FOR SEQ ID NO: 4:
SEQUENCE CHARACTERISTICS:
LENGTH: 1415 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: 81ngle
Query Match
Best Local Similarity
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                                                                                                                                        PEATURE:

NAME/KEY: misc_feat
LOCATION: 1275...128
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                      TOPOLOGY: linear MOLECULE TYPE: DNA HYPOTHETICAL: NO ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08090
FILING DATE: 19920922
FILING DATE: 19920922
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ATTORNEY/AGENT INFORMATION:
NAME: PABSE, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMI
REFERENCE/DOCKET NUMBER: OMI
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Tang, J. N.
TITLE OF INVENTION: Fusic
TITLE OF INVENTION: Aids
NUMBER OF SEQUENCES: 15
                                                                                                                                                                                                                                                                               ORIGINAL SOURCE:
ORGANISM: Homo sapien
TISSUE TYPE: epithelial
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MEDIUM TYPE: Floppy disk
                                                                                                                            FEATURE:
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CITY: Atlanta
STATE: Georgia
                                                                     NAME/KEY: misc_feature LOCATION: 1410..1415
OTHER INFORMATION: /no
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COUNTRY: U.S.
ZIP: 30303
                                                                                                       NAME/KEY:
                                                                                                                                                                                                               LOCATION: 1..6 OTHER INFORMATION: /note=
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1275..1280
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   43.4%;
99.8%;
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                                                                                                                                            /note=
                                                                       /note= "Restriction
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 Score 624.4; DB 5; Pred. No. 5.5e-138;
                                                                                                                                                                                                               "Restriction
                                                                                                                                            "Restriction
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                Length 1415;
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COUNTRY: U.S.

ZIP: 30303
COMPUTER READABLE FORM:
MEDLIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US92/08090
FILING DATE: 1920922
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Pabst, Patrea L.

#1.25

CITY: Atlanta STATE: Georgi STREET:

Georgia Y: U.S.

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RESULT 3
PCT-US92-08090-3
PCT-US92-08090-3
PCT-US92-08090-3
PSEQUENCE 3, Application PC/TUS9208090
PSEQUENCE TAMPATION:
PAPPLICANT: Tang, J. N.
PITLE OF INVENTION: Fusion Protein TITLE OF INVENTION: Aids
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                   NUMBER OF SEQUENCES: 15
CORRESPONDENCE ADDRESS:
ADDRESSEE: Kilpatrick
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
LENGTH: 1421 base pairs
TYPE: NUCLEIC ACID
STRANDENNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Matches 625;
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Best Local Similarity
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 404-572-6509
TELEPHONE: 404-572-6509
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ORIGINAL SOURCE:
ORGANISM: Homo sapien
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LOCATION: 1416..14
OTHER INFORMATION:
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LOCATION: 1275..1280
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ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
                                                                                                                    CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT 480
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                                                                       AAAAACATACAGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC 540
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Pred. No. 5.5e-138;
0; Mismatches 1;
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PCT-US92-08090-2
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                                                                                                Query Match
Best Local S
Matches 625
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INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Pabet, Patrea L.
REGISTRATION UNMBER: 31,284
REFERENCE/DOCKET NUMBER: OWRF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 404.572-6508
                                                                                                                                                                               FEATURE:

NAME/KEY: misc_feature
LOCATION: 1444..1448
OTHER INFORMATION: /not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0,
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                        FEATURE:
                                                                                                                                                                                                                                                                                                                                                                         TISSUE TYPE:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                           ORIGINAL SOURCE:
ORGANISM: Homo sapien
                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear MOLECULE TYPE: DNA HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM: MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Tang, J. N.
TITLE OF INVENTION: Fusion TITLE OF INVENTION: Aids
                                                                                                                                                                                                                                                                                                                                                                                                                                          ANTI-SENSE:
                                                                                                                                                                                                                                                     OTHER INFORMATION:
                                                                                                                                                                                                                                                                   NAME/KEY: misc_feature
LOCATION: 1275..1280
                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature LOCATION: 1..6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 1448 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: POFILING DATE: 19920922
                                                                                                                Match 43.4%;
Local Similarity 99.8%;
                                                                                                                                                                                                                                                                                                                        OTHER INFORMATION: /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ZIP: 30303
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: Atlanta
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE:
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 61
                                   18
                               ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCCAACTGGCGCTCCTCCCA 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GTGCTAGCTTTCCAGAAGGCCTCCGG 626
 GCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAAAAAAAGGGGATACAGTGGAACTGACC 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Application PC/TUS9208090
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7: U.S.
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100 Peachtree Street
                                                                                                                                                                                                                                                                                                                                                                                                                                            NO
                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                                                         Epithelial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Fusion Protein Genes for Treatment
                                                                                                                                                                                    /note= "Restriction site"
                                                                                                                                                                                                                                                     /note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PCT/US92/08090
                                                                                                    0;
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                                                                                                Score 624.4; DB 5;
Pred. No. 5.5e-138;
0; Mismatches 1;
                                                                                                                                                                                                                                                       "Restriction site"
                                                                                                                                                                                                                                                                                                                          "Restriction site"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Version
                                                                                                    Indels
                                                                                                                                 Length 1448;
                                                                                                    0;
                                                                                                    Gaps
                                                                                                    0
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GENERAL INFORMATION:
APPLICANT: Littman, Dan R.
APPLICANT: Kwon, Douglas S.
APPLICANT: Kwon, Douglas S.
APPLICANT: Won Kooyk, Yvette
APPLICANT: Geijtenbeck, Theo
TITLE OF INVENTION: METHODS OF USING A FACIL
TITLE OF INVENTION: CELLS
FILE REFERENCE: 1049-1-017
CURRENT APPLICATION NUMBER: US/09/517,605
CURRENT FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 17
SOPTWARE: Patentin Ver. 2.0
SEQ ID NO 7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              RESULT 5
US-09-517-605-7
                                                                                                                                         Query Match 43.4%;
Best Local Similarity 99.8%;
Matches 625; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 7, Application US/09517605 Patent No. 6391567
                                                                                                                                                                                                               TYPE: DNA
ORGANISM: Homo sapiens
-09-517-605-7
                                                                                                                                                                                                                                                                  LENGTH: 1742
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                   GCAGCCACTCAGGGAAAGAAGTGGTGCTGGGCAAAAAAGGGGGATACAGTGGAACTGACC 120
                                                                      ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA
                                                                                          ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA
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                                                                                                                                       Score 624.4; DB 3;
Pred. No. 5.8e-138;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                     Sequence (September 1977)

Patent No. 6607879

GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
APPLICANT: Susan G. Stuart
APPLICANT: Susan G. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THE D
TITLE OF INVENTION: EXPRESSION
NUMBER OF ESQUENCES: 1508
CORRESPONDENCE ADDRESS:
ADDRESSE: INCYTE PHARMACEUTICALS, INCORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            RESULT 6
US-09-023-655-1013
; Sequence 1013, Ap
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                                                                                                                                                  STREET: 3174 PORTER DRIVE
CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
COUNTRY: USA
ZIP: 94304
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS
SOFTWARE: Word Perfect 5.2
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/023,655
FILING DATE: HEREWITH
CTACETETTATION:
                                                                                 CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
ATTORNEY/AGENT INFORMATION:
NAME: Zeller, Karen J.
REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  436
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   PA-0001
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RESULT 7
PCT-US92-08090-1
; Sequence 1, Application; GENERAL INFORMATION:
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LIBRARY: GENBANK
CLONE: g179143
US-09-023-655-1013
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 10:
SEQUENCE CHARACTERISTICS:
LENGTH: 1742 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 625; Conservative
                                    APPLICANT: Tang, J. N.
TITLE OF INVENTION: Fusion Protein Genes
TITLE OF INVENTION: Aids
             NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELECOMMUNICATION INFORMATION:
  ADDRESSEE:
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(650) 845-477
Kilpatrick & Cody
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Pred. No. 5.8e-138;
0; Mismatches 1;
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                                                   for Treatment
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; NAME/KBY: misc_feature
; LCCATION: 2460..2465
; OTHER INFORMATION: /note= "Restriction site"
PCT-US92-08090-1
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NAME: Pabet, Patrea L.
REGISTRATION NUMBER: 31,284
REFERENCE/DOCKET NUMBER: OMRF
TELECOMMUNICATION INFORMATION:
TELEPAL: 404-572-6508
TELEPAL: 404-572-655
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2465 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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Best Local Similarity 99.8%;
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ANTI-SENSE: NO.
ORIGINAL SOURCE:
ORGANISM: Homo sapien
ORGANISM: Epithelial
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MOLECULE TYPE: DNA
MOLECULE TYPE: NO
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NAME/KEY: misc_feature
LOCATION: 1.6
LOCATION: 1.6
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COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FEATURE:
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0,
CURRENT APPLICATION DATA;
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CITY: Atlanta
STATE: Georgia
COUNTRY: U.S.
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                                                                                                                                  GACTCAAGAAGAAGCCTTTGGGACCAAGGAAACTTCCCCCCTGATCATCAAGAATCTTAAG
CTAGTGTTCGGATTGACTGCCAACTCTGACACCCCACCTGCTTCAGGGGCAGAGCCTGACC
                                                                                                                                                                                                TGTACAGCTTCCCAGAAGAAGAGAGCATACAATTCCACTGGAAAAAACTCCAACCAGATAAAAG
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                                                                                                                                                                                                                                           TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCAACCAGATAAAG
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                                                                                                              GACTCAAGAAGAAGCCTTTGGGACCAAGGAAACTTCCCCCTGATCATCAAGAATCTTAAG
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Pred. No. 6.4e-138;
D; Mismatches 1;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    "Restriction
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RESULT 8
US-08-284-391B-28
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 Best Local Similarity
                                                                                                                                                                                                               APPLICATION NUMBER: US/08/284,391
FILING DATE: 02-AUG-1994
CLLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
APPLICATION NUMBER: 35,238
REGISTRATION NUMBER: 35,238
REGISTRATION NUMBER: 35,238
REGISTRATION NUMBER: 00786/24
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION: APPLICANT: Seed,
                                                                                                                                                              INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: BATAPOUT, BABAK
APPLICANT: BATAPOUT, BABAK
APPLICANT: ROMEO, Charles
APPLICANT: KOlanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ZIP: 02110
COMPUTER READABLE FORM:
                                                                         MOLECULE TYPE:
                                                                                                    LENGTH: 1304 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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                                                                                          TOPOLOGY:
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Score 622.8; DB 2;
Pred. No. 1.3e-137;
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                 Length 1304;
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US-09-218-950-28
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Patent No. 6284240
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APPLICANT: Romeo, Charles
APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
Andresse: Clark & Elbing LLP
                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION: APPLICANT: Seed,
                 ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
 APPLICATION NUMBER:
                                                                                                                                           COUNTRY:
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 US/09/218,950
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TOPOLOGY: linear
MOLECULE TYPE: CDNA
US-09-218-950-28
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Best Local Similarity 99.7
Matches 624; Conservative
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SEQUENCE CHARACTERISTICS:
LENGTH: 1304 base pairs
TYPE: nucleic acid
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REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00.
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
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ATTORNEY/AGENT INFORMATION:
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GTGCTAGCTTTCCAGAAGGCCTCCGG 626
                                                    ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
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Pred. No. 1.3e-137;
0; Mismatches 2;
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US-08-394-388A-28
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GENERAL INFORMATION:
APPLICANT: Seed, Brian
APPLICANT: Banapour, Babak
APPLICANT: Romeo, Charles
APPLICANT: Romeo, Charles
APPLICANT: Rolanus, Waldemar
APPLICANT: Rolanus, Waldemar
APPLICANT: ROLANIS OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
                                                                                                                                                                                                   Matches 624;
                                                                                                                                                                                                                   Query Match
Best Local Similarity
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APPLICATION NUMBER: US/08/284,39:
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/24
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                        INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/394,388A
FILING DATE: 24-FEB-1995
CLASSIFICATION: 514
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ZIP: 02110
COMPUTER READABLE FORM:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
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                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
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                                                                                                                                                                                               Score 622.8; DB 4;
Pred. No. 1.3e-137;
0; Mismatches 2;
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RESULT 11
US-08-417-495-2
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Patent No. 5843728
GENERAL INFORMATION:
APPLICATION NUMBER: US/08/417,495
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08/203,866
FILING DATE:
APPLICATION NUMBER: US/07/847,566
FILING DATE:
APPLICATION NUMBER: 07/665,961
FILING DATE: March 7, 1991
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 30,022
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Seed, Brian Continue of INVENTION: Redirection of INVENTION: Receptor of Politics: 27
                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 507 or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version
SOFTWARE: Wordperfect (Version 5.0)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENČE ADDRESS:
ADDRESSEE: Fish & Richardson
STREET: 225 Franklin Street
CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                             STATE: MA
COUNTRY: USA
ZIP: 02110-2804
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TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1389 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
US-08-417-495-2
               ; Sequence 2, Application US/08284391
Patent No. 5851828
; GENERAL INFORMATION:
APPLICANT: Seed, Brian
APPLICANT: Banapour, Babak
APPLICANT: Romeo, Charles
APPLICANT: KOlanus, Waldemar
ITILE OF INVENTION: TARGETED CY
TITLE OF INVENTION: CELLS BY CH
NUMBER OF SEQUENCES: 53
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Best Local Similarity
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     CORRESPONDENCE ADDRESS:
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ilarity 99.7%;
Conservative
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Pred. No. 1.3e-137;
0; Mismatches 2;
                                   CYTOLYSIS OF HIV-INFECTED CHIMERIC CD4 RECEPTOR- BEA
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                                   BEARING CELLS
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SEQUENCE CHARACTERISTICS:
LENGTH: 1389 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
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Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 08/195
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 514
PRIOR APPLICATION DATA:
PRIOR APPLICATION NUMBER: 08/195,395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: FastSEQ for Windows Version CURRENT APPLICATION DATA: APPLICATION UNMERE: US/08/284,391B FILING DATE: 02-AUG-1994
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatil
OPERATING SYSTEM: DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
STREET: 17
CITY: Bost
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
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                                                                             CTAGTGTTCGGATTGACTGCCAACTCTGACACCCCACCTGCTTCAGGGGCCAGAGCCTGACC
                                                                                                          ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGTGCAATTG
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176 Federal Street
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PE: cDNA
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99.7%; Pred. No. 1.3
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; TYPE: nucleic acid STRANDEDNESS: double ; TOPOLOGY: linear ; MOLECULE TYPE; CDNA US-09-218-950-2
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US-09-218-950-2
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 Best Local Similarity 99. Matches 624; Conservative
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                                     Query Match
                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/284,39:

PILING DATE: 02-AUG-1994

APPLICATION NUMBER: 08/195,395

FILING DATE: 14-FEB-1994

APPLICATION NUMBER: 07/847,566

FILING DATE: 06-MAR-1992

APPLICATION NUMBER: 07/665,961

FILING DATE: 07-MAR-1991

APPLICATION NUMBER: 07/665,961

FILING DATE: 07-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Elbing, Karen L

REGISTRATION NUMBER: 35,238

REGISTRATION NUMBER: 35,238
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APPLICANT: Seed, Brian
APPLICANT: Banapour, Babak
APPLICANT: Romeo, Charles
APPLICANT: KOlanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                       INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
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COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 00
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
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SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/218,950 FILING DATE: CLASSIFICATION:
                                                                                                                                                                                                                          TELEFAX: 617-428-7045
TELEX:
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99.7%;
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Score 622.8; DB 3;
Pred. No. 1.3e-137;
0; Mismatches 2;
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                                 Length 1389;
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RESULT 14
US-08-394-388A-2
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APPLICANT: Seed, BI
APPLICANT: Banapoul
APPLICANT: Romeo, (
APPLICANT: KOlanus)
                                                                                                                                                                                                                                                                                                                                     Sequence 2, Application Patent No. 6753162
        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
COMPUTER: IBM COMPATIBLE
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION NUMBER: US/08/394,388A
FILING DATE: 24-FEB-1995
                                                                                                                                                                NUMBER OF SEQUENCES: 53
CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
CITY: Boston
                                                                                                                                                                                                                                     APPLICANT: Banapour, Babak
APPLICANT: Romeo, Charles
APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING
                                                                                                                                     STATE: M
CLASSIFICATION:
                                                                                                                           ZIP: 02110
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Best Local
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/247001
TELECHONE: 617-428-0200
TELEPAX: 617-428-7045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 1389 base pairs
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APPLICATION NUMBER:
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les 624; Conserv
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                GTGCTAGCTTTCCAGAAGGCCTCCGG
                                                                                                                               AAAAACATACAGGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC
                                                                                                                                                                    CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT
                                                                                                                                                                                      CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT
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                                                                                                                                                                                                                                                                                                 ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGAGGTGCAATTG
                                                                                                                                                                                                                                                                                                                                                                                                               TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCAACCAGATAAAG
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 GTGCTAGCTTTCCAGAAGGCCTCCAG
                                                      ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
                                                                       ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
                                                                                                            AAAAACATACAGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                43.2%;
ilarity 99.7%;
Conservative
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Pred. No. 1.3e-137;
0; Mismatches 2;
 626
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Sequence 2, Application:
GENERAL INFORMATION:
APPLICANT: The General Hospital Corporation
TITLE OF INVENTION: Redirection of Cellular Immunity by Receptor
TITLE OF INVENTION: Chimeras
NUMBER OF SEQUENCES: 27
CORRESPONDENCE 19th & Richardson
STREET: 225 Franklin Street
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PCT-US92-01785-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ; MOLECULE TYPE:
PCT-US92-01785-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Sim
Matches 624;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TELEFAX: (617) 542-8906
TELEX: 200154
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
LENGTH: 1389 base pairs
TYPE: NUCLEIC ACID
STRANDEDNUSS: double
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM PC. DOS (Version 3.30)
SOFTWARE: Wordperfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION UNMER: PCT/US92/01785
FILING DATE: 19920306
CLASSIFICATION BATA:
APPLICATION UNMBER: 07/665,961
FILING DATE: 19920306
PRIOR APPLICATION NUMBER: 07/665,961
APPLICATION NUMBER: 07/665,961
APPLICATION NUMBER: 07/665,961
FILING DATE: MARCH 7, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/119002
TELECOMMUNICATION INFORMATION:
         301
                                                        241
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                                                                                     GACTCAAGAAGAAGCCTTTGGGACCAAGGAAACTTCCCCCCTGATCATCAAGAATCTTAAG
                                                                                                                                                                          TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCAACCAGATAAAG
                                                                                                                                                                                                                                                                                                                                    GCAGCCACTCAGGGAAACAAAGTGGTGCTGGGCAAAAAAAGGGGATACAGTGGAACTGACC
                                                                                                                                                                                                                                                                                                                                                              GCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAAAAAAGGGGGATACAGTGGAACTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                                              ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCCCA
ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGTGCAATTG
                                                        GACTCAAGAAGAAGCCTTTGGGACCAAGGAAACTTCCCCCTGATCATCAAGAATCTTAAG
                                                                                                                                               TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCAACCAGATAAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          43.2%; Score 622.8; DB 5; 99.7%; Pred. No. 1.3e-137; tive 0; Mismatches 2;
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ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGTGCAATTG

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                                                                      ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAAATAGACATCGTG
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                                                                                                                                                                                CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT
                                                                                                                                                                                                                                       CTAGTGTTCGGATTGACTGCCAACTCTGACACCCTGCTTCAGGGGCAGAGCCTGACC
GTGCTAGCTTTCCAGAAGGCCTCCAG
                         GTGCTAGCTTTCCAGAAGGCCTCCGG 626
                                                                                                                                                                CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT
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                                                                                                           ANANACATACAGGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC
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Search completed: November 22, 2004, 14:15:34 Job time: 143 secs

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Run on:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              November 22, 2004, 12:51:30 ; Search time 774 Seconds (without alignments) 10053.253 Million cell updates/sec
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1440
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| (gn2_6/ptodata/2/pubpna/US07_PUBCOMB.seq:*
| (gn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
| (gn2_6/ptodata/2/pubpna/US06_NEW_PUB.seq:*
| (gn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
| (gn2_6/ptodata/2/pubpna/US06_PUBCOMB.seq:*
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Copyright (c) 1993 - 2004 Compugen Ltd.
/ Cgm2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
/ Cgm2_6/ptodata/2/pubpna/US09B_PUBCOMB.seq:*
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/ Cgm2_6/ptodata/2/pubpna/US09C_PUBCOMB.seq:*
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/ Cgm2_6/ptodata/2/pubpna/US10D_PUBCOMB.seq:*
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/ Cgm2_6/ptodata/2/pubpna/US10E_PUBCOMB.seq:*
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/ Cgm2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
/ Cgm2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
/ Cgm2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
/ Cgm2_6/ptodata/2/pubpna/US10_NEW_PUB.seq:*
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/cgn2_6/ptodata/2/pubpna/PCTUS_PUBCOMB.seq:*
                                                                                                                                                                                                                                                                                                                                                                                                                                                    6/ptodata/2/pubpna/US08_NEW_PUB.seq:*
6/ptodata/2/pubpna/US08_PUBCOMB.seq:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

												Result No.
12	11	10	9	80	7	σ	ம	4.	w	N	_	No.
622.8	622.8	622.	622.8	622.8	622.8	622.8	624.4	624.4	624.4	624.4	625	Score
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43.2	43.2	43.2	43.2	43.2	43.2	43.2	43.4	43.4	43.4	43.4	43.4	Query Match
1728	1728	1599	1599	1389	1389	1304	1742	1742	1377	1377	8911	% Query Match Length
11	10	11	10	11	10	10	16	14	15	14	16	DB
US-09-243-008-1	US-09-939-537-1	US-09-243-008-3	US-09-939-537-3	US-09-243-008-2	US-09-939-537-2	US-09-939-537-28	US-10-641-643-1013	US-10-151-274-7	US-10-188-444-38	US-10-103-597A-38	US-10-612-192-3	ID
Sequence 1, Appli	Sequence 1, Appli	Sequence 3, Appli	Sequence 3, Appli	Sequence 2, Appli	Sequence 2, Appli	Sequence 28, Appl	Sequence 1013, Ap	Sequence 7, Appli	Sequence 38, Appl	Sequence 38, Appl	Sequence 3, Appli	Description

5	44	43	42	41	40	39	38	37	36	35	კ 4	33	32	31	30	29	28	27	26	25	24	23	22	21	20	19	18	17	16	15	14	13
401	401	408.6	428.6	463.2	534	μ	535.6	35.	41.	42	549.4	552.2	552.2	552.2	7.	607.4		612	612	612.2	612.2	612.2	612.2	613.4	•	•			621.2		622.8	622.8
27.8	27.8	28.4	29.8.	32.2	37.1	37.2	37.2	37.2	37.6	37.7	38.2	38.3	38.3	38.3	39.7	42.2	42.3	42.5	42.5	42.5	42.5	42.5	42.5	42.6	42.6	43.1	43.1		43.1		43.2	
900	720	723	741	792	534	2159	2159	1769	2379	563	1113	1508	1508	1508	573	719	609	2482	2482	11228	3273	1149	1149	1796	1796	1416	1416	1416	1273	3084	1745	1742
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10-203-754	US-10-151-882-10	US-10-151-882-9	10-322-673-	US-10-422-628-13	US-09-934-060A-25	-09-934-060A-	US-09-934-060A-1	9-934-060A-	10-073-118-	-118-	US-09-759-841-5	US-10-769-247-5	10	10-157-40	10-024-32	US-09-939-537-30	US-10-466-836-24	US-09-766-995-3	US-08-485-163-4	10-	US-10-397-569-7	US-09-766-995-5	US-08-485-163-6	US-09-766-995-1	US-08-485-163-2	-10-769	-10-097	-10-157	09-891	-10-207-655-1	-10-024-32	US-09-891-119A-8
e 37	5		71,	Sequence 13, Appl	25,	ω	1,	2	N	ი 2	'n	s	s	ம	w	30,	e 2	u	Α,	Sequence 6, Appli	e 7	ູຫ	თ	Н	N						Sequence 1, Appli	Sequence 8, Appli

ALIGNMENTS

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; OTHER INFORMATION: Expression Vector PTK13+Neo4 US-10-612-192-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 1
US-10-612-192-3
                                                                                                                                                                                                                                     NUMBER OF SEQ ID NOS: 3
SOFTWARE: PatentIn version 3.2
SEQ ID NO 3
  Query Match
Best Local Similarity
Matches 625; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Pal,
APPLICANT: Mark
APPLICANT: Keer
APPLICANT: Whit
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 3, Application US/10612192 Publication No. US20040076636A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/10/612,192
CURRENT FILING DATE: 2003-07-02
PRIOR APPLICATION NUMBER: US 09/905,962
PRIOR FILING DATE: 2001-07-17
PRIOR APPLICATION NUMBER: US 09/479,675
PRIOR FILING DATE: 2000-01-07
PRIOR FILING DATE: 2000-01-07
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Whitney, Stephen
APPLICANT: Kalyanaraman, V.S.
TITLE OF INVENTION: HIV Immunogenic Complexes
FILE REFERENCE: 00711 CIP
                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: US 09/075,544 PRIOR FILING DATE: 1998-05-11
                                                                                                                                        TYPE: DNA
ORGANISM: Artificial
FEATURE:
                                                                                                                                                                                                            LENGTH: 8911
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Keen, Timothy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                al, Ranajit
Markham, Phillip
43.4%; Score 625; DB 16; I ilarity 100.0%; Pred. No. 5.6e-171; Conservative 0; Mismatches 0;
                                           Length 8911;
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Indels

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Gaps

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; TYPE: DNA
; ORGANISM: Homo sapiens
; FEATURE:
; NAME/KEY: CDS
; LOCATION: (1)...(1377)
US-10-103-597A-38
                                                                                                                                                                                                                                         Sequence 38, Application US/10103597A
Publication No. US20030096432A1
GENERAL INFORMATION:
APPLICANT: Jakobsen, Bent Karsten
TITLE OF INVENTION: Screening Methods
FILE REFERENCE: 102286.142
CURRENT APPLICATION NUMBER: US/10/103,597A
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: PCT/BB00/03579
PRIOR APPLICATION NUMBER: GB 9922352.1
PRIOR APPLICATION NUMBER: GB 9922352.1
PRIOR PILING DATE: 1099-09-21
JUNDER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 2
US-10-103-597A-38
                     Query Match
Best Local Similarity
Matches 625; Conserv
                                                                                                                                                                                                                              LENGTH: 1377
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                   43.4%;
milarity 99.8%;
Conservative
                     Score 624.4; DB 14; Length 1377; pred. No. 4.5e-171; 0; Mismatches 1; Indels 0;
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                                                                                 ; TYPE: DNA; ORGANISM: Homo sapiens; FEATURE; FEATURE; NAME/KEY: CDS; LOCATION: (11...(1377) US-10-188-444-38
                                                                                                                                                                                                APPLICATION NUMBER: GB 9922352.1
PRIOR FILING DATE: 199.99-92
PRIOR APPLICATION NUMBER: GB 9922352.1
PRIOR APPLICATION NUMBER: GB 9922352.1
PRIOR FILING DATE: 1999-09-21
PRIOR FILING DATE: 1999-09-21
PRIOR APPLICATION NUMBER: GB 9922352.1
PRIOR FILING DATE: 1999-09-21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 3
US-10-188-444-38
15-50-188-444-38
; Sequence 38, Application US/10188444
; Publication No. US20030104635A1
; GENERAL INFORMATION:
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  Conservative
                   43.4%;
Score 624.4; DB 15;
Pred. No. 4.5e-171;
0; Mismatches 1;
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                                      Length 1377;
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APPLICANT: Kwon, Douglas S.
APPLICANT: Kwon, Douglas S.
APPLICANT: Van Kooyk, Yvette
APPLICANT: Van Kooyk, Yvette
APPLICANT: Geijtenbeck, Theo
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTH
TITLE OF INVENTION: CELLS
FILE REFERENCE: 1049-1-017
CURRENT APPLICATION NUMBER: US/10/151,274
CURRENT APPLICATION NUMBER: US/09/517,605
PRIOR FILLING DATE: 2000-03-02
NUMBER: OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 7
TENCTU: 1742
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                                                                                                                                                                                                                                                          Sequence 7, Application US/10151274 Publication No. US20030064071A1 GENERAL INFORMATION:
                                   LENGTH: 1742
TYPE: DNA
ORGANISM: Homo &
S-10-151-274-7
Query Match
Best Local Similarity
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43.4%;
99.8%;
Score
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624.4; DB 14;
No. 4.9e-171;
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Sequence 1013, Application US/10641643

Publication No. US20040077003A1

GENERAL INFORMATION:
APPLICANT: Cocks, Benjamin G.
Susan G. Stuart
Jeffrey J. Seilhamer
TITLE OF INVENTION: COMPOSITION FOR THI
UNMBER OF SEQUENCES: 1508
COMPUTER READABLE FORM:

MEDIUM TYPE: Floyd disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: WOR'D Perfect 6.1 for Windows/MS-DOS

CURRENT APPLICATION NUMBER: US/10/641,643

APPLICATION NUMBER: US/10/641,643
                                                                                                                                                                                                                                                                       CORRESPONDENCE ADDRESS:
ADDRESSEE: INCYTE PHARMACEUTICALS,
                                                                                                                                                                               CITY: PALO ALTO
STATE: CALIFORNIA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GTGCTAGCTTTCCAGAAGGCCTCCGG 626
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PRIOR APPLICATION DATA:

CLASSIFICATION: <Unknown>

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Best Local Similarity
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REGISTRATION NUMBER: 37,071
REFERENCE/DOCKET NUMBER: PA-0001 US
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 845-4166
INFORMATION FOR SEQ ID NO: 1013:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: <Unknown>
FILING DATE: <Unknown>
ATTORNEY_AGENT_INFORMATION:
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SEQUENCE DESCRIPTION: SEQ ID NO: 1013
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                   GTGCTAGCTTTCCAGAAGGCCTCCGG 626
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                                                                                                                          AAAAACATACAGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC
                                                                                                                                              AAAAAACATACAGGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC
                                                                                                                                                                                         CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCCTCAGTGCAATGTAGGAGTCCAAGGGGGT
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GTGCTAGCTTTCCAGAAGGCCTCCAG
                                                              ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
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STRANDEDNESS: single
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99.8%;
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RESULT 6

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TOPOLOGY: 11near

HOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID
US-09-939-537-28
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                                                                                                                                                                                                                                                                             Matches
                                                                                                                                                                                                                                                                                                   Best
                                                                                                                                                                                                                                                                                                               Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 28:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICATION NUMBER: 08/284,391
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/24
                                                                                                                                                                                                                                                                              Local Similarity
1es 624; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: PASTSEQ for Windows Version CURRENT APPLICATION DATA; PAPLICATION NUMBER: US/09/939,537 FILING DATE: 24-Aug-2001 CLASSIFICATION: <Unknown> PRIOR APPLICATION DATA; PARIOR APPLICATION DATA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
TELEFAX: 617-428-7045
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MEDIUM TYPE: Diskette
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APPLICANT: Seed, Brian
Banapour, Babak
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291
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              TGTACAGCTTCCCAGAAGAAGAACATACAATTCCACTGGAAAAACTCCAACCAGATAAAG
                                                                                                                                       GCAGCCACTCAGGGAAACAAAGTGGTGCTGGGCAAAAAAAGGGGGATACAGTGGAACTGACC
                                                                                                                                                           GCAGCCACTCAGGGAAAGAAGTGGTGCTGGGCAAAAAAAGGGGGATACAGTGGAACTGACC
                                                                   TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCAACCAGATAAAG
                                                                                                                                                                                                           ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA 170
                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: single
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 ATTCTGGGAAATCAGGGCTCCTTCTTAACTAAAGGTCCAACCTGAACGTGAATGATCGCGCT
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ZIP: 02110
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                                                                                                                                                                                                                                                                                                                                                                                                                                                       LENGTH: 1304 base pairs
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ilarity 99.7%;
Conservative
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Romeo, Charles
Rolanus, Waldemar
KOLANUS, WALGEMED CYTOLYSIS OF HIV-INFECTED
CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
                                                                                                                                                                                                                                                                              0,
                                                                                                                                                                                                                                                                             Score 622.8; DB 10, Pred. No. 1.3e-170; 0; Mismatches 2;
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RESULT 7
US-09-939-537-2
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Publication No. US20030138410A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GENERAL INFORMATION
                                                                                       APPLICATION NUMBER: 08/284,391
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/247001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:

MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Banapour, Babak
Romeo, Charles
Kolanus, Waldemar
TITLE OF INVENTION: TARGETED
                                                                                                                                                                                                                                                                PRIOR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Seed, Brian
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                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/09/939,537
FILING DATE: 24-Aug-2001
CLASSIFICATION: cUnknown>
RAPPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY: USA
ZIP: 02110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  STATE: MA
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                                                                                                                                                                                   RESULT 8
US-09-243-008-2
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                                                                                                                                               Sequence 2, Application US/09243008 Publication No. US20040005334A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 624; Conserv
                                                                                GENERAL INFORMATION:
APPLICANT: Seed, Brian et al.
TITLE OF INVENTION: Redirection of Cellular Immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
NUMBER OF SEQUENCES: 40
CORRESPONDENCE ADDRESS:
CORRESPONDENCE ADDRESSE: Fish & Richardson
STREET: 225 Franklin Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: cDNA
SEQUENCE DESCRIPTION: SEQ ID
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1389 base pairs
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                                                                        Receptor Chimeras
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Pred. No. 1.3e-170;
0; Mismatches 2;
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Best Local Similarity 99.7%;
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SEQUENCE CHARACTERISTICS:
LENGTH: 1389 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/394,176
FILING DATE: SEPTEMBER 11,1995
APPLICATION NUMBER: 08/203,866
FILING DATE: February 28, 1994
APPLICATION NUMBER: 07/847,566
FILING DATE: March 6, 1992
APPLICATION NUMBER: 07/665,961
FILING DATE: March 7, 1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version
SOFTWARE: Wordperfect (Version 5.0)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Karen F. Lech, Ph.D REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/270001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: US/09/243,008 FILING DATE: 02-Feb-1999 PRIOR APPLICATION DATA:
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                                                                                     361 CTAGTGTTCGGATTGACTGCCAACTCTGACACCCCACCTGCTTCAGGGGCAGAGCCTGACC 420
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CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT
                                                                                                                                                               ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGTGCAATTG
                                                                                                                                                                                                                      GACTCAAGAAGCCTTTGGGACCAAGGAAACTTCCCCCCTGATCATCAAGAATCTTAAG
                                                                                                                                                                                                                                             GACTCAAGAAGAAGCCTTTGGGACCAAGGAAACTTCCCCCCTGATCATCAAGAATCTTAAG
                                                                                                                                                                                                                                                                                                      ATTCTGGGAÄÄTCÄGGGCTCCTTCATAACTÄÄAGGTCCATCCAAGCTGAATGÄTCGCGCT
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STRANDEDNESS: double
                                                             CTAGTGTTCGGATTGACTGCCAACTCTGACACCCACCTGCTTCAGGGGGCAGAGCCTGACC
                                                                                                                                           ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGTGCAATTG
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; MOLECULE TYPE: cDNA; SEQUENCE DESCRIPTION: SEQ ID NO: US-09-939-537-3
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US-09-939-537-3
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Publication No. US20030138410A1
GENERAL INFORMATION:
APPLICANT: Seed, Brian
Query Match
Best Local Similarity
Matches 624; Conserv
                                                                                                                                                                                                               TELEX: <Unknown>
INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                             PRIOR DATE: 24-Aug-2001
CLASSIFICATION NUMBER: US/09/939,537
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: 08/284,391
FILING DATE: 02-Aug-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 04-Aug-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REGISTRATION NUMBER: 35,238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
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                                                                                                                                                       LENGTH: 1599 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
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COUNTRY: USA
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                                                                                                                   TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         CITY: Boston
                                                                                                                                                                                                                                                                          TELEFAX: 617-428-7045
                                                                                                                                                                                                                                                                                              TELEPHONE: 617-428-0200
  Conservative
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INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
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Romeo, Charles
                  43.2%;
Score 622.8; DB 10;
Pred. No. 1.4e-170;
0; Mismatches 2;
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                                    Length 1599;
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RESULT 10
US-09-243-008-3
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Publication No. US20040005334A1
GENERAL INFORMATION:
APPLICANT: Seed, Brian et al.
                                             COUNTRY: USA
ZIP: 02110-2804
COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3...
SOFTWARE: Wordperfect (Version 5.0)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/243,008
FILING DATE: 02-Feb-1999
                                                                                                                                                                                                                                                           CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
                                    PRIOR
                                                                                                                                                                                                                                                                                                                    NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                               TITLE OF INVENTION: Redirection of Cellular Immunity Receptor Chimeras
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                                                                                                                                                                                                                              CITY: Boston
STATE: MA
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APPLICATION NUMBER: US/08/394,176 FILING DATE: SEPTEMBER 11,1995
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Best Local Similarity
Matches 624; Conserv
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INFORMATION FOR SEQ ID NO: 3:
SEQUENCE CHARACTERISTICS:
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FILING DATE: February 28, 1994
APPLICATION NUMBER: 07/847,566
FILING DATE: March 6, 1992
APPLICATION NUMBER: 07/665,961
FILING DATE: March 7, 1991
ATTORNEY/AGENT INFORMATION:
NAME: Karen F. Lech, Ph.D
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 07/86/27
TELECHONE: (617) 542-5070
TELEPHONE: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: linear MOLECULE TYPE: DNA (genomic) SEQUENCE DESCRIPTION: SEQ ID NO:
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                                  GTGCTAGCTTTCCAGAAGGCCTCCAG
                                                        GTGCTAGCTTTCCAGAAGGCCTCCGG
                                                                                                                                                                                           AAAAACATACAGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC
                                                                                                                                                                                                                                                                 CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT
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TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                    ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
                                                                                                                                     ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
                                                                                                                                                                                                                                           CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT
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Pred. No. 1.4e-170;
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US-09-939-537-1
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Publication No. US20030138410A1
GENERAL INFORMATION:
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                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: «Unknown»
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1728 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CURRENT APPLICATION NUMBER: US/09/939,537

FILING DATE: 24-Aug-2001

FILING DATE: 24-Aug-2001

CLASSIFICATION: CUnknown>
PRIOR APPLICATION DATA:

APPLICATION DATA:

APPLICATION DATA:

APPLICATION NUMBER: 08/284,391

FILING DATE: 02-AUG-1994

APPLICATION NUMBER: 08/195,395

FILING DATE: 14-FEB-1994

APPLICATION NUMBER: 07/847,566

FILING DATE: 06-MAR-1992

APPLICATION NUMBER: 07/865,961

FILING DATE: 07-MAR-1991

ATTORNEY/AGENT INFORMATION:

NAME: Elbing, Karen L

REGISTRATION NUMBER: 35,238

REFERENCE/DOCKET NUMBER: 00786/247001

TELEPHONE: 617-428-0200

TELEPAX: 1840-020
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Seed, Brian
Banapour, Babak
Romeo, Charles
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                                                                    121 TGTACAGCTTCCCCAGAAGAAGAACAATTCCACTGGAAAAAACTCCCAACCAGATAAAG
                                                                                                                                                                                                                                                624;
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GCAGCCACTCAGGGAAACAAAGTGGTGCTGGGCAAAAAAGGGGGATACAGTGGAACTGACC
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                                                                                                                                                                                                 ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA
                                                                                                                                                                                                                                                                                                                                            TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
TUPE: cDNA
                                                TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCAACCAGATAAAG
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COUNTRY: USA
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INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
CELLS BY CHIMERIC CD4 RECEPTOR- BE
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Pred. No. 1.4e-170;
0; Mismatches 2;
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RESULT 12
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Publication No. US20040005334A1
GENERAL INFORMATION:
APPLICANT: Seed, Brian et al.
INFORMATION FOR SEQ ID NO: 1:
                                                      COMPUTER READABLE FORM:

COMPUTER READABLE FORM:

MEDIUM TYPE: 3.5" Diskette, 1.44 Mb

COMPUTER: IBM PS/2 Model 50Z or 55SX

OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)

SOFTWARE: Wordperfect (Version 5.0)

CURRENT APPLICATION NUMBER: US/09/243,008

FILING DATE: 02-Feb-1999

PRIOR APPLICATION NUMBER: US/08/394,176

FILING DATE: SEPTEMBER 11,1995

APPLICATION NUMBER: 07/08/394,766

FILING DATE: February 28, 1994

APPLICATION NUMBER: 07/865,961

FILING DATE: March 7, 1991

APPLICATION NUMBER: 07/665,961

FILING DATE: March 7, 1991

ATTORNEY/AGENT INFORMATION:

REFERENCE/DOCKET NUMBER: 00786/270001

TELEPAN: (617) 542-5070

TELEPAN: (617) 542-5070
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Fish & Richardson P.C.
STREET: 225 Franklin Street
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COUNTRY: USA
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                                         TELEFAX: (617) 542-8906
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
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LENGTH: 1728 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
SEQUENCE DESCRIPTION: SEQ ID NO
US-09-243-008-1
Sequence 8, Application US/09891119A
Publication No. US20040013683A1
GENERAL INFORMATION:
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: DERIVATIVES OF SOLUBLE T-
FILE REFERENCE: 24577-CY-B
CURRENT APPLICATION NUMBER: US/09/891,119A
CURRENT FILING DATE: 2001-06-25
NUMBER OF SEQ ID NOS: 22
SOFTWARE: Patentin version 3.1
SEQ ID NO 8
SEQ ID NO 8
LENGTH: 1742
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Pred. No. 1.4e-170;
0; Mismatches 2;
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                                                                                                                                  Sequence 1, Application US/10024329
Publication No. US20030157063A1
GENERAL INFORMATION:
APPLICANT: SANHADJI, Kamel
APPLICANT: TOURAINE, Jean-Louis
APPLICANT: LEROY, Pierre
APPLICANT: MEHTALI, Majid
TITLE DEFERRACE, 100002
FITE DEFERRACE, 100002
                                            FILE REFERENCE: 109993
CURRENT APPLICATION NUMBER: US/10/024,329
CURRENT FILING DATE: 2001-12-21
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 1
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LENGTH: 1745
TYPE: DNA
ORGANISM: human
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Pred. No. 1.4e-170;
0; Mismatches 2;
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; ORGANISM: Homo sapiens
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                                                                                                                                           Sequence 169, Application US/10207655

Publication No. US20030118592A1

GENERAL INFORMATION:
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUSION PROTEINS
FILE REFERENCE: 390069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SEQ ID NO 169
SEQ ID NO 169
                                                   Query Match
Best Local
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Best Local Similarity
                                       Matches
                                                                                                                                   LENGTH: 3084
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Similarity 99.7%;
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Pred. No. 1.7e-170;
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Pred. No. 1.4e-170;
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Maximum Match 100%
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ALIGNMENT

REFERENCE AUTHORS TITLE Ş SOURCE ORGANISM 망 Ś 밁 Ś 吊 RESULT 1
CD609192/c
LOCUS
DEFINITION
ACCESSION
VERSION
KEYWORDS ORIGIN COMMENT FEATURES Matches 624; Query Match JOURNAL source Local Similarity 181 121 726 61 GCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAAAAAAAGGGGGATACAGTGGAACTGACC Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Butheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 783)
1 (bases 1 to 783)
1 (circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK CD609192 783 bp mRNA linea 5606991J1 FLP Homo sapiens cDNA, mRNA sequence CD609192 GI:40257455 Incyte Genomics, Inc. 3160 Porter Dr., Palo Alto, CA 94304, USA Tel: 6508454102 Homo sapiens (human) ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTGCTGGTGCTGCAACTGGCGCTCCTCCCA 60 TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCAACCAGATAAAG Conservative gfu@incyte.com. /organism="Homo sapiens"
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1 (bases 1 to 932)

Li,W.B., Gruber,C., Jessee,J. and Polayes,D.

Full-length cDNA libraries and normalization

NL Unpublished (2001)

On May 15, 2003 this sequence version replaced gi:30787731.

Contact: Genoscope

Genoscope - Centre National de Sequencage

BP 191 91006 EVRY cedex - France

Email: seqrefagenoscope.cns.fr, Web : www.genoscope.cns.fr

1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.

This sequence belongs to sequence cluster 6485.r

For more information about this cluster, see

http://www.genoscope.cns.fr/cdna?s=CSODE002AD01QP1&c=6485.r.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
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Homo sapiens PLACENTA Homo
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the Not I and EcoRV sites of the pCMVSPORT 6 vector.
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; HC
B 1 (bases 1 to 816)
S NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collectic
Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LI
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                                                                                                                                                                                                                                                                                BI838409
603083373F1 NIH_MGC_120
                                                                                                                                                                                  Homo sapiens
                                                                                                                                                                                                     Homo sapiens (human)
                                                                                                                                                                                                                      BI838409.1
EST.
                                                                                                                                                                                                                                                     mRNA sequence.
BI838409
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Pred. No. 2.5e-152;
0; Mismatches 2;
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sapiens cDNA
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IMAGE:5222323 5',
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; Homo.
      (LLNL)
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540 659 480 599 420 539 360 479 300 419 359 180 120 239 60

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FEATURES

source

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EST 05-MAY-2004 CS0CAP006YP07

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623;
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Clone distribution: MGC clone distribution information
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
plate: LLAM11559 row: b column: 20
High quality sequence stop: 803.
Location/Qualifiers
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                    GGTGCTAGCTTTCCAGAAGGCCTCCGG 626
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GGTGCTAGCTTTCCAGAAGGCCTCCAG
                                                                                                           CACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGT
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/note="Organ: pooled pancreas and spleen; Vector:
/note="Organ: pooled pancreas and spleen; Vector:
pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of spleen and pancreas from 28 yo
male. Library is oligo-dT primed and directionally cloned
(EcoRV site is destroyed upon cloning). Average insert
size 1.5 kb, insert size range 1-2.5 kb. Library is
normalized and enriched for full-length clones and was
constructed by C. Gruber (Invitrogen). Research Genetics
tracking code 025. Note: this is a NIH_MGC Library."
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/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5222323"
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AUTHORS
TITLE
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KEYWORDS
SOURCE
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Matches 622;
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BX457159
5-PRIME,
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This sequence belongs to sequence cluster 6485.r
For more information about this cluster, see
http://www.genoscope.cns.fr/cdna?s=CSOCAP006CH04QP1&c=6485.r.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was constructed by Life Technologies, a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 (bases 1 to 822)
Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 22, 2003 this sequence version replaced
Contact: Genoscope
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Genoscope - Centre National de S
BP 191 91006 EVRY cedex - France
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Mammalia; Eutheria;
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                        GATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGAGGAGTACTT
                                                                                                                                                                   ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA
GATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGTGCAATT
                                                                                                             TGACTCAAGAAGAAGCCTTTGGGACCAAGGAAACTTCCCCCCTGATCATCAAGAATCTTAA
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                                                                                  TGACTCAAGAAGAAGCCTTTGGGACCAAGGAAACTTTCCCCCTGATCAACAAGAATCTTAA
                                                                                                                                                                                                                                                     CTGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCAACCAGATAAA
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/clone_Tib="Homo sapiens THYMUS"
/clone_Tib="Homo sapiens THYMUS"
/note="Vector: pcMVSPORT 6; lst strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned :
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
Library was not normalized."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Pred. No. 3.4e-146;
L; Mismatches 2;
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Query Match Best Local

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                                            622;
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
      1 ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA
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NIH-MGC http://mgc.nci.nih.gov/
National Institutes of Health, /
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/note="Organ: pooled brain, lung, testis; Vector:
/note="Organ: pooled brain, lung, testis; Vector:
pcMV-SPORT6; Site 1: Not!; Site 2: ECORV (destroyed); RNA
source anonymous pool of 6 male brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (ECORV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
                                                                                                                                                                                                                                                                                                                                                                      /organism="Homo Bapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
/clone="IMAGE:5180642"
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JOURNAL
Email: Cgapbs-Temail.nih.gov

Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1159 row: m column: 20
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High quality sequence start: 11
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Cocation/Qualifiers
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NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
Unpublished (1999)
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603041415F1 NIH MGC_115 Homo
mRNA sequence.
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                                                                                                                                      GG-TGCTAGCTTTCCAGAAGGCCTTCCGGA 627
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                                                                                                                                                                         CACCTGGACATGCACTGTCTTGCAGAACCAGACGAAGGTGGAGTCCAACATAGACATCGT
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/mol_type="mRNA"
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/clone="IMAGE:5226427"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone
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Pred. No. 1.9e-143;
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                             bp mRNA linear EST 04-OCT-20
sapiens cDNA clone IMAGE:5182274 5',
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Best Local
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Tissue Procurement: Life Technologies, Inc.
cDNA Library Preparation: Life Technologies, Inc.
cDNA Library Arrayed by: The I.M.A.G.B. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.B. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM11454 row: n column: 03
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (1999)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 791)
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                       GCTAGTGTTCGGATTGACTGCCAACTCTGACACCCCACCTGCTTCAGGGGCAGAGCCTGAC
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GCTAGTGTTCGGATTGACTGCCAACTCTGACACCCACCTGCTTCAGGGGCAGAGCCTGAC
                                                                                                                   GATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGAGGATT
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                                                                                           GATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGTGCAATT
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/note="Organ: pooled brain, lung, testis; Vector:.
/note="Organ: pooled brain, lung, testis; Vector:.
pCMV-SPORT6; Site_1: Not1; Site_2: EcoRV (destroyed); RNA
source anonymous pool of 6 male_brains, age range 23-27; 1
male lung, age 27; and 1 male testis, age 69. Library is
oligo-dT primed and directionally cloned (BcoRV site is
destroyed upon cloning). Average insert size 1.8 kb,
insert size range 1-3 kb. Library is normalized and
enriched for full-length clones and was constructed by C.
Gruber (Invitrogen). Research Genetics tracking code
021. Note: this is a NIH_MGC Library."
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/db_xref="taxon:9606"
/clone="IMAGE:5182274"
/lab_host="DH10B"
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Pred. No. 2.1e-140;
0; Mismatches 1;
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BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr Web: www.genoscope.cns.fr
1st strand cDNA was primed with a NotI-oligo(dT) primer. Five prime
end enriched, double-strand cDNA was digested with Not I and cloned
into the Not I and EcoRV sites of the pCMVSPORT 6 vector. Library
was not normalized. Library was constructed by Life Technologies, a
division of Invitrogen.
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Li,W.B., Gruber,C., Jessee,J. and Polayes,D.
Full-length cDNA libraries and normalization
Unpublished (2001)
On May 15, 2003 this sequence version replaced
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 5-PRIME,
BX437619
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   This sequence belongs to sequence cluster 6485.r For more information about this cluster, see http://www.genoscope.cns.fr/cdna7s=CSOCAP007DB01QP1&c=6485.r.
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/clone="CSOCAPOO7YDO2"
/clone=Lype="MIXMUS"
/tissue type="MIXMUS"
/tissue type="MIXMUS"
/clone lib="Homo sapiens THYMUS"
/clone lib="Homo sapiens THYMUS"
/clone lib="Homo sapiens THYMUS"
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
/note="Vector: pCMVSPORT 6; 1st strand cDNA was primed
with a NotI-oligo(dT) primer. Five prime end enriched,
double-strand cDNA was digested with Not I and cloned into
the Not I and EcoRV sites of the pCMVSPORT 6 vector.
- '\----' "as not normalized."
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/mol_type="mRNA"
/db_xref="taxon:9606"
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Primates;
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Pred. No. 2.5e-130;
1; Mismatches 1;
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CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL)
DNA Sequencing by: Incyte Genomics, Inc.
Clone distribution: MGC clone distribution information can
found through the I.M.A.G.E. Consortium/LLNL at:
http://image.llnl.gov
Plate: LLAM1626 row: j column: 03
High quality sequence stop: 717.
                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Life Technologies, Inc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Unpublished (1999)
Contact: Robert Strausberg, Ph.D.
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1 (bases 1 to 723)

NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, Mammalian Gene Collection (MGC)
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/clone_lib="NIH_MGC_121"
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/note="Organ: brain; Vector: pCMV-SPORT6; Site_1: NotI;
Site_2: ECORV (destroyed); RNA source anonymous pool of fetal brains, female age 20 weeks, female age 24 weeks and male age 26 weeks. Library is oligo-dT primed and directionally cloned (ECORV site is destroyed upon
                                                                                                                                         /organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleost.
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 679)
Pu,G.K., Wang,J.T., Yang,J., Au-Young,J. and Stuve,L.L.
Circular rapid amplification of cDNA ends for high-throughput extension cloning of partial genes
Genomics 84 (1), 205-210 (2004)
Contact: Fu GK
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                  3160 Porter Dr.,
Tel: 6508454102
                                           Incyte Genomics,
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    gfu@incyte.com
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Contact: Takao Isogai
Genomics Laboratory
Helix Research Institute
1532-3 Yana, Kisarazu, Chi
Tel: 81-438-52-3975
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                                                                       Isogai,T.
HRI human cDNA project
Unpublished (2000)
                                                                                                               Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (Dases 1 to 732)

Ota,T., Nishikawa,T., Suzuki,Y., Ishii,S., Saito,K., Kawai,Y.,
Yamamoto,J., Wakamatsu,A., Nakamura,Y., Nagai,T., Sugano,S. and
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/mol type="mRNA"
/db xref="rtaxon:9606"
/clone lib="FLP"
/note="Vector: pDrive Clo
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Pred. No. 9.2
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                                                                                                        AGENCOURT 26517764 NIH MGC 212 Homo sapiens cDNA clone IMAGE:30974065 5', mRNA sequence. CO246446 CO246446.1 GI:49111174
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Fax: 81-438-52-3986
Email: genomics@hri.co.jp
HRI human cDNA project; 5'- & 3'-end one pass sequencing: Helix
Research Institute; cDNA library construction: Department of
Virology, Institute of Medical Science, University of Tokyo, and
1 (bases 1 to 754)
NIH-MGC http://mgc.nci.nih.gov/.
National Institutes of Health, M
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Location/Qualifiers
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Mammalia; Eutheria;
                                                                              Homo
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/tissue_type="thyroid gland"
/clone_lib="THYRO1"
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/db_xref="taxon:9606"
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            of Health, Mammalian Gene
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Pred. No. 4e-121;
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Query Match
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DNA Sequencing by: Agencourt Bioscience Corporation
Clone distribution: MGC clone distribution information can be found through the I.M.A.G.E. Consortium/LLNL at:
http://image.lnl.gov
Plate: NDAM1165 row: o column: 18
High quality sequence stop: $07.
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Bldg. 31 Rm.10A07 Bethesda, MD 20892
Email: cgapbs-r@mail.nih.gov
Tissue Procurement: Mary Hendrix
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Contact: Daniela S. Gerhard, Ph.D
Office of Cancer Genomics
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/lab host="DH108 (TI phage resistant)"
/clome_lib="NIH MGC_212"
/clome_lib="NIH MGC_212"
/note="Organ: Lung; Vector: pYX-Asc; Site_1: EcoR I;
/note="Organ: Lung; Vector: pYX-Asc; Senome Research, 6:791-806,
196. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with Oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Not I and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is GATAAGGCCA. Tissue was provided by Mary Hendrix."
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Pred. No. 4.1e-117;
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University of Iowa
375 Newton Road , 4156 MEBRF, Iowa City, IA 52242, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          710 bp mRNA linear UI-HF-ELO-avo-e-23-0-UI.rl NIH_MGC_212 Homo sapiens IMAGE:30563734 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Contact: Soares, MB
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 710)
Bonaldo, M.F., Lennon, G. and Soares, M.B.
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CF125444.1 GI:33201679
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: bento-soares@uiowa.edu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 cDNA Library preparation: Dr. M. Bento Soares, University of Iowa CDNA Library Arrayed by: Dr. M. Bento Soares, University of Iowa DNA Sequencing by: Dr. M. Bento Soares, University of Iowa Clone Distribution: Distribution information can be found at http://genome.uiowa.edu/distribution/humanfl.html
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TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAAACTCCAACCAGATAAAG 180
                                          GCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAAAAAAAGGGGATACAGTGGAACTGACC
                                                                                                                                      ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA
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                                                                                                                                                                                                                                                                                                                  /db xrer="caxous:3000"
/clone="IMAGE:30563734"
/tissue_type="Chondrosarcoma Lung Metastasis cell lines"
/lab host="DH108 (T1 phage resistant)"
/clone_lib="NIH MGC_212"
/clone_lib="NIH MGC_212"
/note="Organ: Lung; Vector: pYX-Asc; Site 1: EcoR I;
Site 2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dr
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Not I and then cloned
directionally into pYX-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is GATAAGGGCCA. Tissue was provided by Mary Hendrix."
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                                                                                                                                                                                                                                                                                                                                             Email: cgapbs-r@mail.nih.gov
CDNA Library Preparation:
CDNA Library Arrayed by: The I.M.A.G.B. Consortiv
DNA Sequencing by: National Institutes of Health
Sequencing Center (NISC)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NISC gl09e06.y1 NCI_CGAP_Lei2 Homo sapiens cDNA clone IMAGE:3290578 5', mRNA sequence.
CB052686
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Unpublished (1997)
Contact: Robert Strausberg, Ph.
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                                                                                                                                                                                                                                                                               info@image.llnl.gov
Plate: LLAM8058 ro
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/clone="IMAGE:3290578"
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/lab_host="DH10B"
                                                                                                                                                                                  organism="Homo sapiens"
/mol_type="mRNA"
/db_xref="taxon:9606"
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National Institutes of Health, Mammali
Unpublished (1999)
Contact: Daniela S. Gerhard, Ph.D.
Office of Cancer Genomics
National Cancer Institute / NIH
Bldg. 31 Rm10A07 Bethesda, MD 20892
Email: cgapbs-remail.nih.gov
Tissue Procurement: Mary Hendrix
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803 bp mRNA linear ES'
AGENCOURT 26527156 NIH MGC 212 Homo sapiens cDNA clone
IMAGE:30921364 5', mRNA sequence.
                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 803)
CDNA Library Preparation: M. Bento Soares, University of CDNA Library Arrayed by: The I.M.A.G.E. Consortium (LLNL) DNA Sequencing by: Agencourt bisocience Corporation Clone distribution: MGC clone distribution information can found through the I.M.A.G.E. Consortium/LLNL at: http://image.llnl.gov plate: NDAM1158 row: O column: 05
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                                                                                          CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT
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Location/Qualifiers
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/lab host="DH108 (T1 phage resistant)"
/clone_lib="NIH_MGC_212"
/clone_lib="NIH_MGC_212"
/clone_lib="NIH_MGC_212"
/site_2: Not I; The library was constructed according
Site_2: Not I; The library was constructed according
Bonaldo, Lennon and Soares, Genome Research, 6:791-806,
1996. Denatured RNA was size fractionated on a 1% agarose
gel. First strand cDNA synthesis was primed with oligo-dT
primer containing a Not I site. Double strand cDNA was
size selected according to mRNA size fraction, ligated
with EcoR I adaptor, digested with Not I and then cloned
directionally into pyx-Asc vector. The library tag
sequence located between the Not I site and the polyA tail
is GATAAGGCCA. Tissue was provided by Mary Hendrix."
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Search completed: November Job time: 4905 secs 22, 14:13:11

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Minimum DB
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Gapop 10.0 , Gapext 0.5
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#H00243 Ig kappa #H00243 Ig kappa #H0026 Ig kappa #H00601 Ig kappa #H00601 Ig kappa #H00608 Ig kappa #H00608 Ig kappa #H00608 Ig kappa #H0060 Ig kappa	109	109	107	109	109	109	107	134	129	108	627	128	109	110	215	95
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A;Reference A;Contents: A;Accession: A;Accession: A;Molecule t; A;Residues: R;Lederman, Mol. Immunol A;Title: A BA;Title: A BA	A,Title: Co. A,Reference A,Reference A,Camerini, Cell 60, 74 A,Title: A, A,Reference A,Reference A,Reference A,Reference A,Residues: B,Residues: B,Residues: B,Residues: B,Residues: B,Carr, S,A J, Biol. Chh J, Title: Pro	RESULT RWHUT4 T-cell C;Spect: C;Spect: C;Date: C;Date: C;Macdes C;Maddo Cell 42 Cell 42 A;Title A;Title A;Acces A;Acces A;Rose A;Rose A;Exper A;Exper		
A; Reference number: A; Contents: disulfid A; Accession: A34194 A; Accession: A34194 A; Accession: A34194 A; Accession: 26-394 « A; Reference number: A; Accession: A53287 A; Reference number: A; Accession: A53287 A; Residues: 250-264 A; Note: sequence ext. A; Note: sequence ext. A; Condicts: A 50-597 A; Title: A human dim A; Reference number: A; Accession: I54176 A; Accession: I54176 A; Accession: I54176	A;Title: Corrected CDA; Reference number: A; Reference number: A; A; Rofemerini, D; Seed, Cell 60, 747-754, 199) A;Title: A CD4 domain A; Reference number: A; A; Reference number: A; A; Accession: A32722 A; Rolecule type: mRNA; Residues: 26-426, 42; A; Residues: 26-426, 42; A; Title: Protein and	surface surface rate nam (es: Homo 28-May- 28-May- 39-104), 93-104), 93-106), 93-107), 93-10		444444 444444 4444444 4444444 444444 4444
A;Reference number: A34194; MUID:90078; A;Contents: disulfide bonds; carbohydra; A;Accession: A34194 A;Accession: A34194 A;Molecule type: protein A;Residues: 26-394 <car> R;Lederman, S.; DeMartino, J.A.; Daught Mol. Immunol. 28, 1171-1181, 1991 A;Title: A single amino acid substitut: A;Reference number: A53287; MUID:92072; A;Recession: A53287 A;Residues: 250-264, "W', 266-280 <led> A;Note: sequence extracted from NCBI ba;Rodersion; M.C.; Gibbs, R.A. Genomics 14, 590-597, 1992 A;Title: A human dimorphism resulting 18, Reference number: I54176; MUID:93052; A;Status: translated from GB/EMBL/DDBJ</led></car>	A;Title: Corrected CD4 sequence. A;Reference number: A90907; MUID A;Contents: annotation; revision R;Camerini, D.; Seed, B. Cell 60, 747-754, 1990 A;Title: A CD4 domain important A;Reference number: A32722; MUID A;Accession: A32722 A;Status: nucleic acid sequence A;Molecule type: mRNA A;Residues: 26-426,428-458 <cam- 21286-21295,="" 264,="" a;title:="" and="" b;carr,="" biol.="" carbohydrat<="" chem.="" foll="" hemling,="" j.="" m.e.;="" protein="" s.a.;="" td=""><td>RESULT 1 RWHUT4 T-cell surface glycoprotein CD4 pr T-cell surface mames: T-cell surface C;Species: Homo sapiens (man) C;Date: 28-May-1986 #sequence revi C;Accession: A90872; A32722; A3419 R;Maddon, P.J.; Littman, D.R.; God Cell 42, 93-104, 1985 R;Match 1985 A;Title: The isolation and nucleot A;Fittle: The isolation and nucleot A;Reference number: A90872; MUID:8 A;Accession: A90872 A;Molecule type: mRNA A;Residues: 1-25,'N',27-458 <mad> A;Coss-references: UNIPROT:PO1730 A;Experimental source: clone pT4B R;Littman, D.R.; Maddon, P.J.; Axe Cell 55, 41 1988</mad></td><td></td><td>11000000000000000000000000000000000000</td></cam->	RESULT 1 RWHUT4 T-cell surface glycoprotein CD4 pr T-cell surface mames: T-cell surface C;Species: Homo sapiens (man) C;Date: 28-May-1986 #sequence revi C;Accession: A90872; A32722; A3419 R;Maddon, P.J.; Littman, D.R.; God Cell 42, 93-104, 1985 R;Match 1985 A;Title: The isolation and nucleot A;Fittle: The isolation and nucleot A;Reference number: A90872; MUID:8 A;Accession: A90872 A;Molecule type: mRNA A;Residues: 1-25,'N',27-458 <mad> A;Coss-references: UNIPROT:PO1730 A;Experimental source: clone pT4B R;Littman, D.R.; Maddon, P.J.; Axe Cell 55, 41 1988</mad>		11000000000000000000000000000000000000
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carl	int lon did	CD4 purface n) ce rev ; \$\overline{\bar{A}}{341}\$ R.; \$\overline{G}{0}\$ mucleo MUID: <max display="block">AMAD> ce pT4B compage pT4B compage pT4B</max>		
ate-bind ate-bind arty, B. erty, B. ion in a s95; PMI transla transla transla transla	A;Title: Corrected CD4 sequence. A;Reference number: A90907; MUID:89028665; PMID:3263213 A;Reference number: A90907; MUID:89028665; PMID:3263213 A;Contents: annotation; revision to residue 26 R;Camerini, D; Seed, B. R;Title: A CD4 domain important for HIV-mediated syncytium A;Reference number: A32722 MUID:90182664; PMID:2107024 A;Reference number: A32722 A;Status: nucleic acid sequence not shown; not compared wit A;Mclecule type: mRNA A;Residues: 26-426,428-458 <cam> R;Carr, S.A.; Hemling, M.E.; Polena-Wasserman, G.; Sweet, F. J. Biol. Chem. 264, 21286-21295, 1989 A;Title: Protein and carbohydrate structural analysis of a</cam>	surface glycoprotein CD4 precursor [validated] rnate names: T-cell surface antigen T4/Leu 3 (les: Homo sapiens (man) 28-May-1986 #sequence revision 31-Dec-1988 #t ssion: A90872; A32722; A34194; A53287; I54176; nn, P.J.; Littman, D.R.; Godfrey, M.; Maddon, D 293-104, 1985 21 The isolation and nucleotide sequence of a c rence number: A90872; MUID:85254948; PMID:29907 ssion: A90872 ule type: mRNA lues: 1-25, NY, 27-458 <mad> lues: 1-25, NY, 27-458 <m< td=""><td>ALIGNMENTS</td><td>\$40379 \$14683 C30608 \$346369 \$38643 PH0965 PH0963 PA30608 P30607 S57444 B30601</td></m<></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad></mad>	ALIGNMENTS	\$40379 \$14683 C30608 \$346369 \$38643 PH0965 PH0963 PA30608 P30607 S57444 B30601
	re to	RESULT 1 RWHUT4 T-cell surface glycoprotein CD4 precursor [validated] - human N;Alternate names: T-cell surface antigen T4/Leu 3 C;Species: Homo sapiens (man) C;Date: 28-May-1986 #sequence_revision 31-Dec-1988 #text_change 09-Jul-2004 C;Accession: A90872; A32722; A33194; A53287; I54176; I54297; A02109; A30039 R;Maddon, P.J.; Littman, D.R.; Godfrey, M.; Maddon, D.E.; Chess, L.; Axel, I Cell 42, 93-104, 1985 A;Title: The isolation and nucleotide sequence of a cDNA encoding the T cell A;Reference number: A90872; MUID:85254948; PMID:2990730 A;Rocession: A90872 A;Molecule type: mRNA A;Residues: 1-25,'N',27-458 <mad> A;Experimental source: Clone pT4B R;Littman, D.R.; Maddon, P.J.; Axel, R. Cell 55 & A1 1048 Cell 55 & A1 1048</mad>		
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R;Hodge, T.W.; Sasso, D.R.; McDougal, J.S.

Hum. Immunol. 30, 99-104, 1991

A;Title: Humans with OKT4-epitope deficiency have a single nucleotide base change in A;Reference number: I54297; MUID:91216786; PMID:1708753

A;Accession: I54297

A;Status: translated from GB/EMBL/DDBJ

A;Molecule type: DNA,

A;Molecule type: DNA,

A;Residues: I-584, W1, 266-458 <RE2>

A;Cross-references: GB:M35160; NID:9179143; PIDN:AAA16069.1; PID:g179144

C;Comment: Macrophage tropic strains of HIV-1 bind to a complex of chemokine (C-C) rec.
                                                                  A;Title: A CD4 domain important for HIV-mediated syncytium A;Reference number: A32722; MUID:90182664; PMID:2107024 A;Accession: B32722 A;Molecule type: mRNA A;Residues: 1-432 <CAM>
A;Cross-references: UNIPROT:P16004; GB:M31135 A;Cross-references: UNIPROT:P16004; GB:M31135 R;Fomsgaard, A.; Hirsch, V.M.; Johnson, P.R. Eur. J. Immunol. 22, 2973-2981, 1992 A;Title: Cloning and sequences of primate CD4 molecules: di A;Reference number: A46534; MUID:93049640; PMID:1425921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T-cell surface glycoprotein CD4 - chimpanzee
N;Alternate names: T-cell surface antigen T4/Leu 3
C;Specias: Pan troglodytes (chimpanzee)
C;Date: 30-Sep-1993 #sequence_revision 30-Sep-1993 #text_change 09-Jul-2004
C;Accession: B32722; A46534
R;Camerini, D.; Seed, B.
Cell 60, 747-754, 1990
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A;Cross-references: GDB:119767; OMIM:186940

A;Cross-references: GDB:119767; OMIM:186940

A;Map position: 12pter-12pt2

A;Introns: 16/3

C;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology C;Keywords: AIDS; duplication; glycoprotein; T-cell; transmembrane protein F;1-25/Domain: signal sequence #status predicted <SIG-F;26-458/Product: T-cell surface glycoprotein CD4 #status experimental <MAT>F;34-11/Domain: immunoglobulin homology <#MI>F;316-186/Domain: immunoglobulin homology #status atypical <IM2>F;316-299/Domain: immunoglobulin homology <IM3>F;321-372/Domain: immunoglobulin homology <IM3>F;321-372/Domain: immunoglobulin homology <IM4>F;321-372/Domain: immunoglobulin homology <IM4
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A;Residues: 1-72 <RES>
A;Cross-references: GB:U47924; GB:M86525; GB:U72506; NID:g1633547; PIDN:AAB51309.1;
R;Hodge, T.W.; Sasso, D.R.; McDougal, J.S.
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F;421-458/Domain: intracellular #status predicted <INT>
F;41-109,155-184,328-370/Disulfide bonds: #status experimental
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A;Status: not
                                            A;Accession: A46534
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compared with conceptual translation
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C;Comment: This protein is expressed on most thymocytes, on a subset of C;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology C;Keywords: duplication; glycoprotein; T-cell; transmembrane protein F;1-432/Product: T-cell surface glycoprotein CD4 #status predicted <MAT> F;1-371/Domain: extracellular #status predicted <EXT> F;1-371/Domain: immunoglobulin homology <IM3> F;111-161/Domain: immunoglobulin homology <IM3> F;180-293/Domain: immunoglobulin homology <IM3> F;296-347/Domain: immunoglobulin homology <IM3
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F;9-86/Domain: immunoglobulin homology <IMJ>
F;111-161/Domain: immunoglobulin homology #status atypical <IM
F;191-274/Domain: immunoglobulin homology <IMJ>
F;296-347/Domain: immunoglobulin homology <IMJ>
F;296-347/Domain: immunoglobulin homology <IMJ>
F;372-395/Domain: immunoglobulin homology <IMJ>
F;372-395/Domain: intransmembrane #status predicted <IMM>
F;376-432/Domain: intracellular #status predicted <INT>
F;16-84,130-159,303-345/bisulfide bonds: #status predicted
F;271,300/Binding site: carbohydrate (Asn) (covalent) #status
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A;Note: sequence extracted from NCBI backbone (NCBIP:118332)
A;Note: sequence extracted from NCBI backbone (NCBIP:118332)
C;Comment: This protein is expressed on most thymocytes, on a subset of C;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology C;Keywords: duplication; glycoprotein; T-cell; transmembrane protein F;1-433/Product: T-cell surface glycoprotein CD4 #status predicted <MAT:
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A;Title: R CD4 domain important for HIV-mediated syncytium formation lies outside the vii A;Reference number: A32722; MUID:90182664; PMID:2107024
A;Accession: C32722
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            T-cell surface glycoprotein CD4 - rheaus macaque
N,Alternate names: T-cell surface antigen T4/Leu 3
C,Species: Macaca mulatta (rheaus macaque)
C,Date: 30-Sep_1993 #sequence_revision 30-Sep-1993 #text_change 16-Jul-1999
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R;Camerini, D.; Seed, B.
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A; Residues: 1-432 < CAM>
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;271,300/Binding site: carbohydrate (Asn) (covalent) #status
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Pred. No. 1.3e-36;
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Pred. No. 4.9e-41;
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RESULT 5
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$41374
Single chain Fv antibody - mouse
C;Species: Mus musculus (house mouse)
C;Date: 06-Jan-1995 #sequence_revision 06-Jan-1995 #text_change
C;Accession: S41374
R;Artseachko, O.; Weiler, E.W.; Muentz, K.; Conrad, U.
submitted to the EMBL Data Library, January 1994
A;Description: Construction and functional characterization of
A;Reference number: S41374
A;Accession: S41374
A;Status: preliminary
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A;Title: A high affinity digoxin-binding protein displayed on A;Reference number: A56446; MUID:95229583; PMID:7713873
A;Accession: A56446
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ig heavy chain V region (3H-3H scFv) - mouse (strain BALB/C) C;Species: Mus musculus (house mouse) C;Date: 19-Jan-1996 #sequence_revision 19-Jan-1996 #text_change C;Accession: A56446
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A56446
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A; Residues: 1-249 < ART>
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C;Keywords: heterotetramer; i
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A; Residues: 1-268 < TAN>
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                A; Cross-references: EMBL: Z29480
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 immunoglobulin
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                                                                                                   single chain
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                                                                                                      7
                                                                                                      antibo
         p53 specific single-chain antibody Pab421 - C;Species: Homo sapiens (man) C;Date: 15-May-1997 #sequence_revision 15-Ma C;Accession: JC5322 R;Jannot, C.B.; Hynes, N.E.
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Biochem.
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C;Accession: A46254
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Best Local Similarity
Matches 136; Conserv
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Best Local
 Biophys. Res.
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A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Molecule type: mRNA
A; Residues: 1-459 < HAG>
A; Residues: 1-459 < HAG>
A; Residues: Terrected from NCBI backbone (NCBIN:112732, NCBIP:112733)
A; Note: sequence extracted from NCBI backbone (NCBIN:112732, NCBIP:112733)
C; Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology
F:322-372/Domain: immunoglobulin homology < IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Hague, B.F.; Sawasdikosol, S.; Brown, T.J.; Lee, K.; Recker, D.P.; Kindt, Proc. Natl. Acad. Sci. U.S.A. 89, 7963-7967, 1992
A;Title: CD4 and its role in infection of rabbit cell lines by human immunou A;Reference number: A46254; MUID:92390370; PMID:1518821
A;Accession: A46254
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ;Species: Oryctolagus cuniculus (domestic rabbit);Date: 21-Sep-1993 #sequence_revision 18-Nov-1994
                                                                                                                                                                                                                                                                                                                                                                              Local Similarity
                                                                                                                                                                                                  ILGNQG----SFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKE 116
                                                                                                                                                                                                                                                              EVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLEL 176
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LAWYQQKPGQAPRLLIYGASTRATGVPARFSGSGSGAEFTLIISSLQSEDFAVYYCQQYN 478
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APHLQGRVTITADKSTSTVYLELRNLRSDDTAVYFCAGVYEGEADEGEYDNNGFLKHWGQ
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QDSGTWSCHLSFQDQNKLELDIKIIVLGFPKAS
                                         ODSGTWTCTV-LONOKKVEFKIDIVVLAFOKAS
                                                                                  EVELLVFRLTANPNTRLLHGQSLTLTLEGPSVGSPSVQWKSPENKIIETGPTCSMPKLRL
                                                                                                                                                                         ILGNOGSSSSSFWLKGNSPLSNRVESKKNMWDQGSFPLVIKDLRMDDSGTYICEVGDKKM 120
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                                                                                                                                                                                                                                                                                                                                                     Score 618.5; DB 2;
Pred. No. 1.7e-25;
4; Mismatches 47;
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Pred. No. 2.5e-28;
0; Mismatches 65
                                         208
213
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230,

242-246, 1997

15-May-1997 human

#text_change

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RESULT 8

330193
T-cell surface glycoprotein CD4 - dog
C;Species: Canis lupus familiaris (dog)
C;Species: Canis lupus familiaris (dog)
C;Species: Con-1995 #sequence_revision 06-Jan-1995 #text_change 21-J
C;Accession: S30193
R;Milde, K.F.; Conner, G.E.; Mintz, D.H.; Alejandro, R.
Biochim. Biophys. Acta 1172, 315-318, 1993
A;Title: Primary structure of the canine CD4 antigen.
A;Reference number: S30193; MUID:93192324; PMID:7916632
A;Accession: S30193
A;Status: preliminary
A;Molecule type: mRNA
A;Residues: 1-432 «MIL»
A;Cross-references: EMBL:X60565; NID:g288652; PIDN:CAB37664.1; PID:C;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homo:C;Keywords: glycoprotein
C;Keywords: glycoprotein
F;202-311/Domain: immunoglobulin homology <IMM>
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Best Local
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                                                                                                                                               ----NSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTW 182
                                                                                                                                                                                   GSSRLKHRVESKKNLWDQGSFPLVIKDLEVADSGIYFCDT-DKRQEVELLVFNLTAKWDS
                                                                                                                                                                                                      GPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTA----
                                                                                                                                                                                                                                                            LMLQLVMLPAVTPVREVVLGKAGDAVELPCQTSQKKN1HFNWRDSSMVQ1LGNQGSFWTV
                                                                                                                                                                                                                                                                             LVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTK 71
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                                                                    TCTVLQNQKKVEFKIDIVVLAFQKAS 208
                                                                                                            GSSSGSSNIRLLQGQQLTLTLENPSGSSPSVQWKGPGNKSKHGGQNLSLSWPELQDGGTW
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                                                                                                                                                                                                                                                                                                                                                  22.3%; Score 596; DB 2; 56.3%; Pred. No. 2.4e-24;
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                                                                                                                                                                                                                                                                                                                                38; Mismatches
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homology
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A27449
T-cell Burface glycoprotein CD4 precursor - rat
T-cell Burface glycoprotein CD4 precursor - rat
N;Alternate names: W3/25 antigen
C;Species: Rattus norvegicus (Norway rat)
C;Date: 21-May-1988 #sequence_revision 21-May-1988 #text_change 09-Jul-2004
C;Accession: A27449; A35433
R;Clark, S.J.; Jefferies, W.A.; Barclay, A.N.; Gagnon, J.; Williams, A.F.
R;Clark, S.J.; Jefferies, W.A.; Barclay, A.N.; Gagnon, J.; Williams, A.F.
R;Coc. Natl. Acad. Sci. U.S.A. 84, 1649-1653, 1987
A;Title: Peptide and nucleotide sequences of rat CD4 (W3/25) antigen: evide
A;Reference number: A27449; MUID:87175535; PMID:3104900
A;Accession: A27449;
                                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: EMBL:X72453; NID:g441374; PIDN:CAA51121.1; PID:g441375 (SUperfamily: immunoglobulin V region; immunoglobulin homology C;Keywords: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;36-110/Domain: immunoglobulin homology <IMM>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     R;Klein, R.; Jaenichen, R.; Zachau, H.G.
Bur. J. Immunol. 23, 3248-3271, 1993
A;Title: Expressed human immunoglobulin chi genes and their
A;Reference number: S40312; MUID:94080891; PMID:8258341
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S40343
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C;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology
C;Keywords: glycoprotein; membrane protein; surface antigen
F;219-300/Domain: immunoglobulin homology <IMM>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C;Date: 19-May-1994 #sequence_revision 26-May-1995 #text_change C;Accession: S40343
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ig kappa chain V-J region - C; Species: Homo sapiens (mar
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A; Residues: 1-457 < CLA>
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                                                                                                                                                                                                    Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 MNRGVPFRHL--LLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQ
                                                                                                                                                                                                                                             Similarity
                                                  ELELTQSPATLSVSPGERATLSCRASESVSSDLAWYQQKPGQAPRLLIYGASTRATGVPA
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EIVMTQSPATLSVSPGERATLSCRASQSVSSNLAWYQQKPGQAPTVLIYGASTRATGIPA
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Pred. No. 9.2e-20;
                                                                                                                                                                                               Score 507; DB 2;
Pred. No. 3.3e-20;
7; Mismatches 3
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RFSGSGSGAEFTLTISSLQSEDFAVYYCQQYNNWPPRYTFGQGTRLEIK 495

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Eur. J. Immunol. 23, 846-851, 1993
A;Title: Nucleotidic sequence analysis of the variable (A;Reference number: S34001; MUID:93209281; PMID:7681398
A;Status.
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Eur. J. Immunol. 23, 3248-3271, 1993
A;Tille: Expressed human immunoglobulin chi genes and their hypermutation.
A;Reference number: S40312; MUID:94080891; PMID:8258341
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C;Species: Homo sapiens (man)
C;Date: 06-Mar-1994 #sequence_revision 26-May-1995 #text_change 21-Jan-2000
C;Accession: S40362
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C;Date: 02-Dec-1993 #sequence_revision 10-Nov-1995 #text_change C;Accession: S34005; S30524
R;Mariette, X; Tsapis, A.; Brouet, J.C.
T-cell surface glycoprotein CD4 precursor - mouse N; Alternate names: T-cell differentiation antigen C; Species: Mus musculus (house mouse)
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                                                                                                                                                               RFSGSGSGAEFTLTISSLQSEDFAVYYCQQYNNWPPRYTFGQGTRLEIK 495
                                                                                                                                                                                                   ELELTQSPATLSVSPGERATLSCRASESVSSDLAWYQQKPGQAPRLLIYGASTRATGVPA
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Pred. No. 8.9e-20;
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Pred. No. 8.2e-20;
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               L3T4;
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             surface antigen T4/Leu
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A;Introns: 18/1; 74/1; 128/1; 207/1; 319/1; 386/1; 425/3; 448/2
C;Superfamily: T-cell surface glycoprotein CD4; immunoglobulin homology
C;Keywords: alternative initiators; duplication; glycoprotein; T-cell; transi
F;1-26/Domain: signal sequence #status predicted sIGs
F;27-457/Product: T-cell surface glycoprotein CD4 #status experimental <MAT>
F;35-114/Domain: immunoglobulin homology <IM1>
F;35-1190/Domain: immunoglobulin homology *ISTATION **
F;3190/Domain: immunoglobulin homology *ISTATION **
F;320-301/Domain: immunoglobulin homology *IM3>
F;241-457/Product: CD4, brain-specific short form #status predicted <BRA>
F;321-372/Domain: immunoglobulin homology <IM4>
F;321-372/Domain: immunoglobulin homology <IM4-372/Domain: immunoglo
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A;Molecule type: protein
A;Residues: 27-43 <CLA>
C;Comment: This protein is expressed on most thymocytes, on a subset of mature T-cells
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A;Cross-references: GB:M36851; NID:g198672; PIDN:AAA39402.1; PID:g554183
A;Cross-references: GB:M36851; NID:g198672; PIDN:AAA39402.1; PID:g554183
A;Classon, B.J.; Tsagaratos, J.; Kirszbaum, L.; Maddox, J.; Mackay, C.R.;
Immunogenetics 23, 129-132, 1986
Immunogenetics 23, 129-132, 1986
A;Title: The L3T4 antigen in mouse and the sheep equivalent are immunoglob A;Reference number: A47642; MUID:86166694; PMID:3082751
A;Accession: A47642
F;395-419/Domain: transmembrane #status predicted <TMM>F;490-457/Domain: intracellular #status predicted <INT>F;420-457/Domain: intracellular #status predicted <INT>F;42-112,159-188,328-370/Disulfide bonds: #status predicted F;42-112,159-188,328-370/Disulfide bonds: #status predicted F;187,298,323,392/Binding site: carbohydrate (Asn) (covalen
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A;Accession: I69018
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A;Title: L3T4 and the immunoglobulin gene superfamily: lA;Reference number: I54564; MUID:88152875; PMID:3326818
A;Accession: I54564
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R;Gorman, S.D.; Tourvieille, B.; Parnes, J.R.
Proc. Natl. Acad. Sci. U.S.A. 84, 7644-7648, 1987
A;Title: Structure of the mouse gene encoding CD4 and an A;Reference number: A39893; MUID:88041159; PMID:2823269
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A; Residues: 1-457 < LIT>
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A; Title: Unusual intron in
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A; Molecule type: DNA
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A; Residues: 25-457 < MAD>
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A; Residues: 1-25, 'E', 27-457 < GOR>
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A; Residues: 1-457 < TOU>
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              in the immunoglobulin domain of 038; MUID:87115821; PMID:3027575
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     (covalent)
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C;Superfamily: in C;Keywords: hete F;16-90/Domain:
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S40378
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C;Date: 05-Jun-1988 #sequence_revision 05-Jun-1988 #text_change 21-Jan-2000
C;Accession: B265555
R;Middaugh, C.R., Litman, G.W.
J. Biol. Chem. 262, 3671-3673, 1987
A;Title: Atypical glycosylation of an IgG monoclonal cryoimmunoglobulin.
A;Reference number: A92630; MUID:87137666; PMID:3102493
                                                                            C; Superfamily: im
C; Keywords: heter
F; 29-103/Domain:
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A;Molecule type: protein
A;Residues: 1-116 <MID>
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                                                                            A;Cross-references: EMBL:X72488; NID:g441444; PIDN:CAA51156.1; PID:g441445 C;Superfamily: immunoglobulin V region; immunoglobulin homology C;Kupwrds: heterotetramer; immunoglobulin C;Keywords: heterotetramer; immunoglobulin F;29-103/Domain: immunoglobulin homology <IMM>
                                                                                                                                                          A;Status: preliminary; translation not shown A;Molecule type: mRNA A;Residues: 1-123 <KLE>
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Query Match
Best Local Similarity
Matches 90; Conserv
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Best Local Similarity
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Best Local Similarity
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18.2%;
ilarity 80.4%;
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10;
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Pred. No. 4e-19;
9; Mismatches
Score 485; DB 2;
Pred. No. 4.4e-19;
LO; Mismatches 12
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Search completed: November 21, 2004, 13:43:29 Job time : 57.6204 secs

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1 MNRGVPFRHLLLVLQLALLP.....GTRLEIKLVPRGSGHHHHHH 508
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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ALIGNMENTS

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Stapleton M., Soares M.B., Bonaido M.F., CaBavant T.L., Scheetz T.B., Brownstein M.J., Usdin T.B., Toshiyuki S., Carninci P., Prange C.,	L., Marusina K., Farmer A.A., Rubin G.M., Hong L.,	, Moore T., Max S.I., Wang J., Hsieh F.	., Buetow K.H., Schaefer C.F., Bhat N	F.S., Wagner L., Shenmen C.M., S	old E.A., Grouse L.H., Derge J.G.,	MEDLINE=22388257; PubMed=12477932; DOI=10.1073/pnas.242603899;	D)	SEQUENCE FROM N.A.		Hum. Immunol. 30:99-104(1991).		substitution of TRP240 fo	"Humans with OKT4-epitope deficiency have a single nucleotide base	D.R., McDougal J.S.;	91216786; PubMed=1708753;	SEQUENCE FROM N.A., AND VARIANT TRP-265.	[4]	Genome Res. 6:314-326(1996).	A Sense fitte transcer les out tresephosphace rechestes	CDA and twicephoenhate	Ansari-Lari M.A., Muzny D.M., Lu J., Lu F., Lilley C.E., Spanos S.,	PubMed=8723724;	•		Cell 55:541-541(1988).	rected CD4 seque	don P.J., Axel	MEDLINE=89028665; PubMed=3263213;	REVISION TO 26.	[2]	•	of the immunoglobulin gene fa	coding the T ce	Maddon P.J., Littman D.R., Godfrey M., Maddon D.B., Chess L., Axel R.;	MEDLINE=85254948; PubMed=2990730;	SEQUENCE FROM N.A.	[1]	D=9606;	Primates: Catarrhini: Hominidae:	Eukarvota: Metazoa: Chordata: Craniata: Vertebrata: Euteleostomi:	ED4;	T4/Leu-3).	F-cell surface glycoprotein the precursor (F-cell surface antigen	-2004 (Rel. 45, Last annotation update)	09, Last	(Rel. 01, Created)	730:	- CD4 HIMAN STANDARD: PRT: 458 AA.	

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DATABASE: NAME=PROW; NOTE=CD guide CD4 entry; WWW="http://www.ncbi.nlm.nih.gov/prow/cd/cd4.htm".

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Crise B., Rose J.K.;

"Identification of palmitoylation sites on CI immunodeficiency virus receptor";

J. Biol. Chem. 267:13593-13597(1992).

-I- FUNCTION: Accessory protein for MHC class receptor interaction. May regulate T-cell.

-I- SUBUNIT: Associates with p56-lck.

-I- SUBCLIULAR LOCATION: Type I membrane pro-
-I- SIMILARITY: Contains 3 immunoglobulin-lik.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Kana S.S., Loquellano N.A., Peters G.J., Abramson R.D., Mullahy S.J., Bosak S.A., McEwan P.J., McKernan K.J., Malek J.A., Gunaratne P.H., Richards S., Worley K.C., Hale S., Garcia A.M., Gay L.J., Hulyk S.W., Villalon D.K., Muzny D.M., Sodergren B.J., Lu X., Gibbs R.A., Fahey J., Helton E., Ketteman M., Madan A., Rodrigues S., Sanchez A., Whiting M., Madan A., Young A.C., Shevchenko Y., Bouffard G.G., Blakesley R.W., Touchman J.W., Green E.D., Dickson M.C., Rodriguez A.C., Grinwood J., Schmutz J., Myers R.M., Schnein J.E., Jones S.J.M., Marra M.A.; "Generation and initial analysis of more than 15,000 full-length human and mouse CDNA secuences."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Carr S.A.,
Barr J.R.,
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MEDLINE=91061882, PubMed=2247146;

Ryu S.-Kwong P.D., Truneh A., Porter T.G., Arthos

Rosenberg M., Dai X., Xuong N.-H., Axel R., Sweet R.W.

Hendrickson W.A.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=91061881; PubMed=1701030; Wang J., Yan Y., Garriett T.P., Liu J., Rodgers D.W., Garlick Tarr G.E., Husain Y., Reinherz E.L., Harrison S.C.; "Atomic structure of a fragment of human CD4 containing two immunoglobulin-like domains.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhang Z., Henzer "., "Signal peptide prediction "Signal peptide prediction verified cleavage sites.", submitted (JUN-2004) to Swi
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[7]
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Fommsgaard A., Hirsch V.M., Johnson P.R.;
"Cloning and sequences of primate CD4 molecules: diversity
cellular receptor for simian immunodeficiency virus/human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (2.4 ANGSTROMS) MEDLINE=91061881; PubMed=1701030;
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Wu H., Kwong P.D., Hendrickson W.
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                                                                                                                                                                                                                                                                                                                                  387:527-530(1997).
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  LOCATION: Type I membrane protein. Contains 3 immunoglobulin-like C2-Contains 1 immunoglobulin-like V-t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             virus.";
22:2973-2981(1992).
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GO; GO:0042289; F:N
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GO:0005866; C:r-cell receptor complex; NAS.
GO:0015026; F:coreceptor activity; NAS.
GO:0015029; F:internalization receptor activity; TAS.
GO:0015029; F:MTC class II protein binding; NAS.
GO:00048289; F:transmembrane receptor activity; TAS.
GO:0004888; F:transmembrane receptor activity; TAS.
GO:0006955; F:immune response; NAS.
GO:0045086; P:positive regulation of interleukin-2 biosyn.
GO:0045086; P:T-cell differentiation; NAS.
GO:0045086; P:T-cell selection; NAS.
GO:0045086; P:T-cell selection; NAS.
GO:0045086; P:T-cell selection; NAS.
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X-ray; A/B=26-388.

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678; CD4.
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Immunoglobulin domain; Lipoprotein; P
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Ig-like C2-type 3.
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N-linked (GlcNAc. .
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Cytoplasmic
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Extracellular
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Best Local Sim
Matches 208;
                                                                                                                                            01-APR-1990 (Rel. 14, Created)
01-APR-1990 (Rel. 14, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
T-cell surface glycoprotein CD4 precursor (T-cell surface antigen T4/Leu-3).
          EMBL; M31135; AAA35407.1; -.
EMBL; X73323; CAA51749.1; -.
PIR; B32722; RWCZT4.
                                                        entities roor send an
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                                                                                                                             This
                                                                                                                                                                                                                                        Fomsgaard A., Hirsch V.M., Johnson P.R.; "Cloning and sequences of primate CD4 molecules: diversity cellular receptor for simian immunodeficiency virus/human
                                                                                                                                                                                                                                                                                                                "A CD4 domain important for HIV-mediated outside the virus binding site."; Cell 60:747-754(1990).
                                                                                                                                                                                                                                                                                                                                                            SEQUENCE FROM N.A.
MEDLINE=90182664; Pub
Camerini D., Seed B.;
                                                                                                                                                                                                                                                                                                                                                                                                                     Pan troglodytes (Chimpanzee).
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Name=CD4;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             P16004;
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                                                                                                                                                                                                                                                                             MEDLINE=93049640; PubMed=1425921;
                                                                                                                                                                                                                                                                                          TISSUE=Blood;
                                                                                                    European
                                                                                                 SWISS-PROT entry is copyright. It is produced through een the Swiss Institute of Bioinformatics and the EN European Bioinformatics Institute. There are no restr
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                                                     pean Bioinformatics Institute. There are no rest non-profit institutions as long as its content and this statement is not removed. Usage by ar requires a license agreement (See http://www.isban email to license@isb-sib.ch).
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Pred. No. 6.2e-59;
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S-palmitoyl cysteine.
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RESULT 3
CD4 MACFA
ID CD4 MACFA
AC P79185;
DT 15-JUL-1998 (K
T 15-JUL-1998 (Re
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T4/Leu-3).
Name=CD4
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PRINTS; PR00692; CD4TCANTIGEN.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Glycoprotein; Immune response; Immunoglobulin domain; Lipoprotein;
Palmitate; Repeat; Signal; T-cell; Transmembrane
STGNAL.
  Macaca fascicularis
Eukaryota; Metazoa;
Mammalia; Eutheria;
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InterPro; IPR000973; CD4_TCAg.
InterPro; IPR007110; Ig-Ilke.
InterPro; IPR003596; Ig_v.
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GO:0012026; F:coreceptor activity; ISS.
GO:0042209; F:MC class II protein binding; ISS.
GO:0006955; P:immune response; ISS.
GO:0005086; P:positive regulation of interleukin-2
GO:0030217; P:T-cell differentiation; ISS.
GO:0045086; P:T-cell selection; ISS.
GO:0045088; P:T-cell selection; ISS.
GO:007169; P:transmembrane receptor protein tyrosi
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                                                                                                                         (Rel. 36, Created)
(Rel. 36, Last sequence update)
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(Rel. 94) (Re
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nilarity 98.1%;
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(Crab eating macaque) (Cynomolgus monkey). Chordata; Craniata; Vertebrata; Euteleostomi; Primates; Catarrhini; Cercopithecidae;
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S-palmitcyl cysteine (
S-palmitcyl cysteine (
T-> N (in Ref. 2).
L-> S (in Ref. 2).
K-> N (in Ref. 2).
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Pred. No. 2e-57;
0; Mismatches
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L -> S (in Ref. 2).
K -> N (in Ref. 2).
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Tatsumi M., Yabe M., Yamada Y.K.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
-I- FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation.
-I- SUBCNIT: Associates with p56-lck (By similarity).
-I- SUBCILIULAR LOCATION: Type I membrane protein.
-I- SUBCILIULAR LOCATION: Type I membrane protein.
-I- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
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SEQUENCE
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PRINTS; PR00692; CD47
SMART; SM00406; IGV;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     InterPro; IPR008424; CD2.
InterPro; IPR000973; CD4 TCAg.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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NCBI_TaxID=9541;
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GO:0015026; F:coreceptor activity; ISS.
GO:0042289; F:MHC class II protein binding; ISS.
GO:0006955; P:immune response; ISS.
GO:0006955; P:positive regulation of interleukin-2 biosyn.
GO:0045086; P:positive regulation; ISS.
GO:0045058; P:T-cell differentiation; ISS.
GO:0045058; P:T-cell selection; ISS.
GO:007169; P:transmembrane receptor protein tyrosine kin.
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Similarity 88.9%;
95; Conservative :
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                                 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
ILGIQGSFLTKGPSKLSDRADSRKSLWDQGCFSMIIKNLKIEDSDTYICEVENKKEEVEL
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                                                                                                                                                                                                                                                                                                                                                                          835; IG_LIKE; 1.
Immune response;
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25
                                                                                                                                                                                                                                                                                                                        50872
                                                                                                                                                                                                                                                                                                             1; T-Cell; Transmembrane.

By similarity.
T-cell surface glycoprotein CD
Extracellular (Potential).

Potential.

Cyroplasmic (Potential).

Ig-like V-type.

Ig-like C2-type 1.

Ig-like C2-type 2.

Ig-like C2-type 3.

N-linked (GlcNAc. . .) (By sim
N-linked (GlcNAc. . .) (By sim)
                                                                                                                                                                                                                                                                                                                        MW.
                                                                                                                                                                                                               12;
                                                                                                                                                                                                         Score 953; DB
Pred. No. 6e-5
12; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Immunoglobulin domain; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (See http://www.isb-sib.ch/announce/
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(By similarity).
(By similarity).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
-!- FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation.
-!- SUBUNIT: Associates with p56-lck (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P79184;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restructe by non-profit institutions as long as its content modified and this statement is not removed. Usage by and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           15-JUL-1998 (Rel. 36, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
                         DOMAIN
DOMAIN
                                                                                           DOMAIN
DOMAIN
                                                                                                                                                                                                                                                                                                                                                       InterPro; IPR008424; CD2.
InterPro; IPR000973; CD4 TCAg.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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Hashimoto O., Tatsumi
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Macaca fuscata fuscata (Japanese macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                        SIGNAL
                                                                                                                                                                                                                                                                     PRINTS; PR00692; CD4;
SMART; SM00406; IGV;
PROSITE; PS50835; IG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 T4/Leu-3).
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                                                                                                                                                                                                                           Palmitate;
                                                                                                                                                                                                                                                  Glycoprotein; Immune
                                                                                                                                                                                                                                                                                                                                      Pfam; PF00047; ig;
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    CARBOHYD
                                                                                                                                       TRANSMEM
                                                                                                                                                          DOMAIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                 GO:0042101; C:T-cell receptor complex; ISS.
GO:0042109; F:coreceptor activity; ISS.
GO:0042209; F:MC class II protein binding; ISS.
GO:0006955; P:immune response; ISS.
GO:0045086; P:positive regulation of interleukin-2
GO:0045086; P:T-cell differentiation; ISS.
GO:0030217; P:T-cell selection; ISS.
GO:0007169; P:transmembrane receptor protein tyrosi
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Potential.
Cytoplasmic (Potent Ig-like V-type.
Ig-like C2-type 1.
Ig-like C2-type 2.
Ig-like C2-type 3.
N-linked (GlcNAc.
                                                                                                                                                                                                      By similarity
                                                                                                                                                          T-cell surface glycoprotein 
Extracellular (Potential).
                                                                                                                                                                                                                                                  Immunoglobulin domain; Lipoprotein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         precursor
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Best Local S
Matches 184
                                                                                                                                                                                                                                                                                                                                                                                                                                                         MACMU
SEQUENCE OF 107-122
SEQUENCE OF 107-122
MEDLINE=98320644; PubMed=9656488,
Harris E.E., Disotell T.R.;
"Nuclear gene trees and the phylogenetic relationships
"angabeys (Primates: Papionini).";
                                                                                                                                                                                                                                                                                                                                                                                        CD4 MACMU STANDARD; PR.1, P.1603; Q29617;
P16003; Q29617;
01-APR-1990 (Rel. 14, Created)
28-FEB-2003 (Rel. 41, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
05-JUL-2004 (Rel. 44, Last annotation update)
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CARBOHYD
DISULFID
DISULFID
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LIPID
                                                                                                   Fomsgaard A., Hirsch V.M., Johnson P.R., "Cloning and sequences of primate CD4 molecules: diversity of the cellular receptor for simian immunodeficiency virus/human immunodeficiency virus.";
                                                                                                                                                                                  TISSUE=Thymocytes;
Hashimoto O., Tatsumi M.;
"Molecular cloning and ex;
Submitted (JUN-1995) to ti
                                                                                                                                                                                                                                               "A CD4 domain important for HIV-mediated outside the virus binding site."; Cell 60:747-754(1990).
                                                                                                                                                                                                                                                                             MEDLINE=90182664;
Camerini D., Seed
                                                                                                                                                                                                                                                                                                                      Cercopithecinae; Macaca.
NCBI_TaxID=9544;
                                                                                                                                                                                                                                                                                                                                        Macaca mulatta (Rhesus macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                         Name=CD4;
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                                                                                                                                            MEDLINE=93049640;
                                                                                                                                                     TISSUE=Blood
                                                                                                                                                               SEQUENCE OF 28-424 FROM N.A.
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                                                                                         virus.";
22:2973-2981(1992)
                                                                                                                                            PubMed=1425921;
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N-linked (GlcNAc...)
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By similarity.
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By similarity.
S-palmitoyl cysteine (
S-palmitoyl cysteine (
M; 76B3E7EF08185535 CRC
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Pred. No. 8
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GO; GO:0042101; C:T-cell receptor complex; ISS.
GO; GO:0015026; F:coreceptor activity; ISS.
GO; GO:0015026; F:coreceptor activity; ISS.
GO; GO:0042289; F:MHC class II protein binding; ISS.
GO; GO:0045055; P:immune response; ISS.
GO; GO:004506; P:Posittve regulation of interleukin-2
GO; GO:0030217; F:T-cell differentiation; ISS.
GO; GO:0045058; P:T-cell selection; ISS.
GO; GO:0045059; P:T-cell selection; ISS.
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PRINTS; PR00692; CD4TCANTIGEN
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG LIKE; 1.
                                                                                                                                                                                                          TIPID
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Palmitate; Repeat; Si
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InterPro; IPR000973; CD4 TCAg.
InterPro; IPR007110; Ig-like.
InterPro; IPR003596; Ig_v.
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EMBL; D63347; BAA09671.1; --
EMBL; X73326; CAA51752.1; --
EMBL; X73326; CAA525129.1;
EMBL; AF057385; AAC25129.1;
HSSP; P01730; 1WBR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation.
-!- SUBUNIT: Associates with p56-lck (By similarity).
-!- SUBCELLULAR LOCATION: Type I membrane protein.
-!- SIMILARITY: Contains 3 immunoglobulin-like C2-type domains.
-!- SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  This SWISS-PROT entry is copyright. It is produced through a collaboratic between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on it use by non-profit institutions as long as its content is in no was been by non-profit institutions as long as its content is in no was
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                                                           Similarity
         MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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                                                                                               Conservative
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                                                                                                           50884
                                                       35.4%;
                                                                                                                                                                                                                                                                                                                                                                                                           response; Immunoglobulin domain; Lipoprotein; ignal; T-cell; Transmembrane.
                                                                                               ¥
                                              13;
                                                                                                      By similarity.
By similarity.
By similarity.
Sysimilarity.
S-palmitoyl cysteine (
S-palmitoyl cysteine (
S-palmitoyl cysteine (
N-> T (in Ref. 1).
L-> S (in Ref. 2).
L-> S (in Ref. 2).
L-> L (in Ref. 2).
S-> P (in Ref. 2).
K-> N (in Ref. 2).
K-> Q (in Ref. 2).
R-> Q (in Ref. 3).
R-> Q (in Ref. 3).
R-> T (in Ref. 2).
                                         Score 945; DB
Pred. No. 1.9e
13; Mismatches
                                                                                                                                                                                                                                                                    Potential.
Cytoplasmic (Potential).
                                                                                                                                                                                                                                                                                                                                                                         Extracellular
                                                                                                                                                                                                                                                                                                                                                                                     T-cell surface
                                                                                               8BB80339FAFEC808
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      receptor protein tyrosine kin.
                                           DB 1; I
..9e-51;
les 12;
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(Potential).
                                                                    Length
                                                                                              CRC64;
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(By similarity)
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(By similarity)
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MNRGIPFRHLLLVLQLALLPAVTQGKKVVLGKKGDTVELTCNASQKKNTQFHWKNSNQIK

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REMBL; D63346; BAADYDO, ...,

REMBL; X73325; CAA51751.1; -.

REMBC; X73325; CAA51751.1; -.

R
CREST CONTRACTOR CONTR
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fonsgaard A., Hirsch V.M., Jöhnson P.R.;

"Cloning and sequences of primate CD4 molecules: diversity of the cellular receptor for simian immunodeficiency virus/human immunodeficiency virus.";

Eur. J. Immunol. 22:2973-2981(1992).

-I- FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation.

-I- SUBUNIT: Associates with p56-lck (By similarity).

-I- SUBCELLULAR LOCATION: Type I membrane protein.

-I- SUMILARITY: Contains 3 immunoglobulin-like C2-type domains.

-I- SIMILARITY: Contains 1 immunoglobulin-like V-type domains.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
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Hashimoto O., Tatsumi M.;
Submitted (FEB-1997) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Macaca nemestrina (Pig-tailed macaque).
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CD4 MACNE STANDARD; PRT; 458 AA.
Q08340; P79196;
01-FEB-1995 (Rel. 31, Created)
15-JUL-1998 (Rel. 36, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
T-cell surface glycoprotein CD4 precursor (T-
T4/Leu-3).
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Name=CD4;
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                                                                                                                                                                                 P:immune response; ISS.
P:positive regulation of interleukin-2
P:T-cell differentiation; ISS.
P:T-cell selection; ISS.
P:transmembrane receptor protein tyrosi
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RESULT 7
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Best Local S
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Q08338; 002805; 077593; Q28217;
Q1-FEB-1995 (Rel. 31, Created)
29-MAR-2004 (Rel. 43, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
T-cell surface glycoprotein CD4 precursor (T-cell
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DISULFID
LIPID
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CARBOHYD
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DOMAIN
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CHAIN
                               Hashimoto O., Tatsumi M. "Molecular cloning and e Submitted (JUL-1996) to
                                                                                                   Cercopithecus aethiops (Green monkey) (Grivet).
Eukaryota; Metazoa; Chordata; Craniata; Vertebr
Mammalia, Eutheria; Primates; Catarrhini; Cerco
Cercopithecinae; Cercopithecus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SEQUENCE
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Palmitate; Rep
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                                                                  SEQUENCE FROM
                                                                                        NCBI_TaxID=9534;
                                                                                                                                                   Name=CD4;
                                                                                                                                                             T4/Leu-3).
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TISSUE=Blood
         EQUENCE OF
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                                                     N.A.
Tatsumi M.;
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         FROM N
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296
325
109
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113
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ignal; T-ce
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By similarity.
By similarity.
By similarity.
S-palmitcyl cysteine (
S-palmitcyl cysteine (
D > N (in Ref. 2).
C -> H (in Ref. 2).
N -> D (in Ref. 2).
D -> E (in Ref. 2).
D -> A (in Ref. 2).
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Ig-like V-type 1.

Ig-like C2-type 2.

Ig-like C2-type 2.

Ig-like C2-type 3.

N-linked (GlCNAC...

N-linked (GlCNAC...
                                EMBL/GenBank/DDBJ
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Pred. No. 2.2e
.4; Mismatches
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Extracellular (Potential).
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T-cell surface
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ell; Transmembrane.
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                                                                                                                           Vertebrata;
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.2e-51;
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                                                                                                               ertebrata; Euteleostomi;
Cercopithecidae;
                                           green monkey CD4.";
                                 databases
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                                                                                                                                                                         surface antigen
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EMBL; D86589; BAA13132.1; -.

RMBL; X73322; CAA51748.1; -.

RR EMBL; AF001226; AAB60873.1; -.

RMBL; AF001228; AAB60875.1; -.

RMBL; AF001228; AAC25124.1; -.

RMBL; AF001228; AAC25124.1; -.

RMSP; P01730; IWIQ.

RGO; GO:0042101; C:T-cell receptor complex; ISS.

RGO; GO:0042101; C:T-cell receptor activity; ISS.

RGO; GO:0042289; F:MFC class II protein binding; ISS.

RGO; GO:0045086; P:positive regulation of interleukin-2 biosyn.

RGO; GO:0045086; P:T-cell differentiation; ISS.

RGO; GO:0045086; P:T-cell selection; ISS.

RGO; GO:0007199; P:T-cell selection; ISS.

RGO; GO:0007199; P:Transmembrane receptor protein tyrosine kin. ...

RR GO; GO:000710; IFR000973; CD4 TCA9.

RINterPro; IPR000973; CD4 TCA9.

R InterPro; IPR0007110; IG-Iike.

R FABM; PF00047; ig; 2.

RR PROSITE; PR00692; CD4TCANTIGEN.

R PROSITE; PS00632; CD4TCANTIGEN.
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Mol. Biol. Evol. 15:892-900(1998).

-i- FUNCTION: Accessory protein for MHC class-II antiger receptor interaction. May regulate T-cell activation receptor interaction. May regulate T-cell activation.

-i- SUBGINIT: Associates with p56-lck (By similarity).

-i- SUBGILIULAR LOCATION: Type I membrane protein.

-i- SUBGILIULAR LOCATION: Type I membrane protein.

-i- SIMILARITY: Contains 1 immunoglobulin-like V-type d.
                                                                                                                                                                                                                         Glycoprotein; Immune response; Palmitate; Repeat; Signal; T-c
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       This SWISS-PROT entry is copyright. It is produced through a collab between the Swiss Institute of Bioinformatics and the EMBL outst the European Bioinformatics Institute. There are no restrictions use by non-profit institutions as long as its content is in modified and this statement is not removed. Usage by and for commodified and this statement is not removed. Usage by and for commodified and this statement is not removed.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MEDLINE=98320644; PubMedd=9656488;
Harris E.E., Disotell T.R.;
"Nuclear con-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fomsgaard A., Hirsch V.M., Johnson P.R.; "Cloning and sequences of primate CD4 molecules: diversity cellular receptor for simian immunodeficiency virus,"; Eur. J. Immunol. 22:2973-2981 (1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fonmsgaard A., Mueller-Trutwin M.C., Diop O., Hansen J., Corbet S., Barre-Sinoussi F., Allan J.S.; Relation between phylogeny of African green monkey CD4 their respective simian immunodeficiency virus genes.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TISSUE=Peripheral blood;
MEDLINE=98017879; PubMed=9379478;
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374
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         Extracellular (Potential).

Potential.

Cytoplasmic (Potential).

Ig-like V-type.
Ig-like C2-type 1.

Ig-like C2-type 2.

Ig-like C2-type 3.

N-linked (GloNAc. . .) (Potential).

N-linked (GloNAc. . .) (Potential).
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T-cell surface glycoprotein
                                                                                                                                                                                                                                       Immunoglobulin domain; Lipoprotein;
                                                                                                                                                                                                                         Transmembrane.
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CD4 CERTO STANDARD;

C08336;

O1-OCT-1996 (Rel. 34, Created)

O1-OCT-1996 (Rel. 34, Last sec

O5-JUL-2004 (Rel. 44, Last and

T-cell surface glycoprotein CI
                                                                                                                                                           Romsgaard A., Hirsch V.M., Johnson P.R.;

"Cloning and sequences of primate CD4 molecules: diversity of the cellular receptor for simian immunodeficiency virus/human immunodeficiency virus.";

Bur. J. Immunol. 22:2973-2981(1992).

FUNCTION: Accessory protein for MHC class-II antigen/T-cell receptor interaction. May regulate T-cell activation.

1. SUBCRIATIAN ACCOMINON: Type I membrane protein.

1. SUBCRIATIAN COCATION: Type I membrane protein.

1. SUBCRIATIAN: Contains 3 immunoglobulin-like C2-type domains.

1. SIMILARITY: Contains 1 immunoglobulin-like V-type domains.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cercopithecinae;
NCBI_TaxID=9531;
[1]
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S-palmitoyl cysteine (
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I-> T (in Ref. 3; AAB
K-> E (in Ref. 3; AAB
M-> V (in Ref. 2 and
F-> L (in Ref. 3; AAB
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T (in Ref. 3; AAB60873).
E (in Ref. 1).
V (in Ref. 3; AAB60873 and 4)
V (in Ref. 2 and 3).
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E (in Ref. 3; AAB60873).
H (in Ref. 3; AAB60873).
AB60873).
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SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
Glycoprotein; Immune response; IC
Palmitate; Repeat; T-cell; Trans
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GO; GO:00042101; C:T-cell receptor
GO; GO:0015026; F:Coreceptor act
GO; GO:0015026; F:MHC class II p
GO; GO:0042289; F:MHC class II p
GO; GO:0042289; F:MHC class II p
GO; GO:0006955; P:Immune respons
GO; GO:00045086; P:Dositive regult
GO; GO:0030217; P:T-cell differer
GO; GO:0030217; P:T-cell selecti
GO; GO:0030217; P:T-cell selecti
GO; GO:007169; P:Transmembrane
InterPro; IPR003974; CD2.
InterPro; IPR00973; CD4 TCA9.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR007110; Ig-Tike.
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GO:0045026; F:coreceptor activity; ISS.
GO:0045289; F:MHC class II protein binding;
GO:0006955; P:immune response; ISS.
GO:0045086; P:positive regulation of interle
GO:0030217; P:T-cell differentiation; ISS.
GO:0030505; P:T-cell selection; ISS.
GO:004505; P:transmembrane receptor proteir
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X73327; CAA51753.1;
P01730; 1WIQ.
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S-palmitoyl cys
S-palmitoyl cys
S-palmitoyl cys
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N-> D.
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V-> M.
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Cytoplasmic (Potential).

Ig-like V-type.

Ig-like C2-type 1.

Ig-like C2-type 2.

Ig-like C2-type 3.

N-linked (GlCNAc...) (IN-linked (GlCNAc...)
                                                                                                                                                                                                                                                                 11;
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Pred. No. 1.2e
11; Mismatches
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                                                                                                                                                                                                                                                                                                                8660B636D2DB38A7 CRC64;
                         397
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l.2e-43;
nes 11;
                                                                                                                                                                                                                                                                                                                                                                                                       cysteine cysteine
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InterPro; IPR008424; C
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InterPro; IPR007110; I
InterPro; IPR003596; I
NON TER
                                     CARBOHYD
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GO; GO:0042101; C:T-cell receptor complex; ISS.

GO; GO:0015026; F:coreceptor activity; ISS.

GO; GO:0015026; F:mHC class II protein binding; ISS.

GO; GO:0042289; F:mHC class II protein binding; ISS.

GO; GO:0006955; P:immune response; ISS.

GO; GO:0045086; P:positive regulation of interleukin-2 biosyn.

GO; GO:0030217; P:T-cell differentiation; ISS.

GO; GO:004508; P:T-cell differentiation; ISS.

GO; GO:004508; P:T-cell selection; ISS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its use by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/or send an email to license@isb-sib.ch).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Fomsgaard A., Hirsch V.M., Johnson P.R.; "Cloning and sequences of primate CD4 molecules: cellular receptor for simian immunodeficiency vii
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           01-FBB-1995 (Rel. 31, Last sequence update)
05-ULL-2004 (Rel. 44, Last annotation update)
T-cell surface glycoprotein CD4 (T-cell surface (Fragment).
                                                                                                                                                                                                                  Glycoprotein;
Palmitate; Re
                                                                                                                                                                                                                                          Pfam; PF00047; 19; 2.
PRINTS; PR00692; CD4TCANTIGEN.
SMART; SM00406; 1Gv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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Mammalia; Eutheria; Primates;
Cercopithecinae; Erythrocebus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Erythrocebus patas
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             immunodeficiency virus.";
Eur. J. Immunol. 22:2973-2981(1992).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TISSUE=Blood
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
                                                                                                   CARBOHYD
                                                                                                                DOMAIN
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                                                                                                                                                                                                       YON TER
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SUBCELLULAR LOCATION: Type I membrane protein.
SIMILARITY: Contains 3 immunoglobulin-like C2-type domain
SIMILARITY: Contains 1 immunoglobulin-like V-type domain.
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391
>397
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; Chordata; Cr
; Primates; Ca
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T-cell; Transmembrane
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Ig-like.
 44081 MW;
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By similarity.
By similarity.
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S-palmitoyl cys
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 67887397A6B7EA4F CRC64;
                                                                                                                                                                                                                              Immunoglobulin domain; Lipoprotein;
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l cysteine
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InterPro; IPR000973; CD4 TCAG.
InterPro; IPR000973; Ig-Tike.
InterPro; IPR003596; Ig v.
Pfam; PP05790; C2-set; Z.
Pfam; PP00047; ig; 1.
PRINTS; PR00692; CD4TCANTIGEN.
SMART; SM00406; IGv; 1.
PROSTITE; PS50835; IG LIKE; 1.
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SEQUENCE
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GO; GO:0016021; C:integral to membrane;
GO; GO:0007155; P:cell adhesion; IEA.
GO; GO:0006955; P:immune response; IEA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., N
Corbet S., Barre-Sinoussi F., Allan J.S.;
"Relation between phylogeny of African green monkey CD4
their respective simian immunodeficiency virus genes.";
J. Med. Primatol. 26:120-128(1997).
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01-JUL-1997 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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                                                                       DQGNFPLIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPP
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86.2%; Pred. No. 1.4e-42;
tive 10; Mismatches 15
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InterPro; IPR00973; CD4 TCA9.
InterPro; IPR009710; Ig-Tike.
InterPro; IPR0031596; Ig v.
Pfam; PF05790; C2-set; Z.
Pfam; PF00047; ig; 1.
PRINTS; PR00692; CD4TCANTIGEN.
SMART; SM00406; IGv; 1.
PROSSITE; PS50835; IG_LIKE; 1.
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CO; GO:00016021; C:integral to membrane;
GO; GO:0007155; P:cell adhesion; IEA.
GO; GO:0006955; P:immune response; IEA.
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NCBI_TaxID=60712;
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Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., I Corbet S., Barre-Sinoussi F., Allan J.S.; "Relation between phylogeny of African green monkey CD4 their respective simian immunodeficiency virus genes."; J. Med. Primatol 26:120-128(1997).
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                           GSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLAFQKA
                                                                                                 DQGCFSMIIKNLKIEDSETYICEVENKKEEVELLVFGLTANSDTHLLQGQSLTLTLESPP
                                                                                                                               DQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPP
GSSPSVKCRSPRGKNIQGGRTLSVPQLERQDSGTWTCTVSQDQNTVEFKIDIVVLAFQKA
                                                                                                                                                                                                        VVLGKKGDTVELTCNASQNTTTQFHWKNSNQIKILGKQGSFLTKGSSKLRDRIDSRKSLW
                                                                                                                                                                                                                                                        WILGKKGDTVELTCTASQKKSIQFHWKNSNQIKILGNQGSFLTKGPSKLNDRADSRRSLW
                                                                                                                                                                                                                                                                                                            30.1%; Score 803; DB 2; larity 86.2%; Pred. No. 1.4e-42; Conservative 10; Mismatches 15
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Last annotation updat
                                                                                                                                                                                                                                                                                                                                                                                                                   CF7F2F5D82335B0D CRC64;
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01-OCT-2003 (TrEMBLrel.

25,

Last

annotation update)

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RESULT 13
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InterPro; IPR00873; CD4 TCA9.
InterPro; IPR00973; CD4 TCA9.
InterPro; IPR007110; Ig-Tike.
InterPro; IPR007110; Ig-Y.
Pfam; PF05790; C2-Bet; Z.
Pfam; PF00692; C2-Bet; Z.
Pfam; PF00692; CD4TCANTIGEN.
SMART; SM00406; IGV; 1.
SMART; SM00406; IGV; 1.
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Q95NE9;
O1-DEC-2001 (TrEI
01-DEC-2001 (TrEI
01-OCT-2003 (TrEI
CD4 (Fragment).
         SEQUENCE FROM N.A.

MEDLINE=98017879; PubMed=9379478;

Fommsgaard A., Muller-Trutwin M.C., Diop O.,

Corbet S., Barre-Sinoussi F., Allan J.S.;
                                                                                                                                                                                                                                                                                                              Name=CD4;
Cercopithecus pygerythrus (Vervet monkey).
Eukaryota; Metazoa; Chordata; Craniata; Ve
Mammalia; Eutheria; Primates; Catarrhini;
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MEDLINE=98017879; PubMed=9379478;

Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., M.

Fomsgaard A., Muller-Trutwin M.C., Diop O., Hansen J., M.

Corbet S., Barre-Sinoussi F., Allan J.S.;

"Relation between phylogeny of African green monkey CD4

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NCBI_TaxID=60712;
[1]
                                                                                                                                                                                                                      NCBI_TaxID=60710;
                                                                                                                                                                                                                                                                                       Cercopithecinae;
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156; Conserv
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nilarity 86.2%;
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(TremBLrel. 19, Last seq
(TremBLrel. 25, Last ann
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                                                                                                                                                                                                                                                                                  Cercopithecus.
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Pred. No. 1.4e
10; Mismatches
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RT their respective simian immunodeficiency virus genes.";

RL J. Med. Primatol. 26:120-128(1997).

R EMBL; AF001223; AAB60870.1; -

DR GO; GO:0016021; C:integral to membrane; IEA.

DR GO; GO:0007155; P:cell adhesion; IEA.

R GO; GO:006955; P:immune response; IEA.

R InterPro; IPR00824; CD2.

R InterPro; IPR00824; CD2.

R InterPro; IPR00973; CD4 TCA9.

R InterPro; IPR003596; Ig v.

R Pfam; PF05790; C2-set; 2.
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EMBL; AP001227; AAB60874 l; -
GO; GO:0016021; C:integral to membrane; IE.
GO; GO:00016025; P:call adhesion; IEA.
GO; GO:0007155; P:immune response; IEA.
InterPro; IPR008424; CD2.
InterPro; IPR000973; CD4 TCAg.
InterPro; IPR000973; CD4 TCAg.
InterPro; IPR000973; CD4 TCAg.
InterPro; IPR0003596; Ig_v.
Pfam; PF05790; C2-set; Z.
Pfam; PF0047; 19; 1.
PRINTS; PR00692; CD4TCANTIGEN.
SMART; SM00406; IGv; 1.
PROSITE; PS50835; IG_LIKE; 1.
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01-JUL-1997 (TrE
01-JUL-1997 (TrE
01-OCT-2003 (TrE
CD4 (Fragment).
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NON_TER
SEQUENCE
                                                                                                                                                     MEDLINE=98017879; PubMed=9379478;
Fomsgaard A., Muller-Trutwin M.C., Diop
Corbet S., Barre-Sinoussi F., Allan J.S.
"Relation between phylogeny of African 9
                                                                                                                                                                                                                                                           Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Cercopithecidae;
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InterPro; IPRO0873; CD4 TCA9.
InterPro; IPRO07110; Ig-Tike.
InterPro; IPRO07110; Ig-Tike.
InterPro; IPRO07110; Ig-Tike.
InterPro; IPRO07596; Ig v.
Pfam; PPO0799; C2-set; Z.
Pfam; PP00799; C2-set; Z.
PRINTS; PR00652; CT4TCANTIGEN.
SMART; SM00406; IGv; 1.
PROSTTE; PS50835; IG_LIKE; 1.
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"Relation between phylogeny of African green monkey CD4 genes a their respective simian immunodeficiency virus genes.";
J. Med. Primatol 26:120-128(1997).
EMBL; AF001224; AAB60871.1; -.
GO; GO:0016021; C:integral to membrane; IEA.
GO; GO:0007155; P:cell adhesion; IEA.
GO; GO:0008955; P:immune response; IEA.
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01-JUL-1997 (TrEMBLrel.
01-OCT-2003 (TrEMBLrel.
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Search completed: November 21, 2004, 13:42:25 Job time: 283.81 secs

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ALIGNMENTS

REFERENCE AUTHORS TITLE SOURCE ORGANISM ACCESSION VERSION KEYWORDS ORIGIN FEATURES DEFINITION JOURNAL source PALL PALENT: JP 2002538814-A 1 19-NOV-2002;

PHE GOVERNMENT OF THE UNITED STATES OF AMERICA AS REPRESENTED BY THE GOVERNMENT OF THE UNITED STATES OF AKTIENGESELLSCHAFT SECRETARY DEPARTMENT OF HEALTH AND HUMAN SERVICES THE NATIONAL INSTITUTES OF HEALTH

OS ARTIficial Sequence
PN 12-002538814-A/1
PD 19-NOV-2002
PF 16-MAR-2000 JP 2000605633
PF 16-MAR-2000 JP 2000605633
PF 16-MAR-1999 US 60/124681
PI EDWARD A BERGER, CHRISTIE DEL CASTILLO
PC C12N15/09, A61X38/00, A61P31/18, C07X5/103, C07X14/00, C07X14/155, PC C07X14/715, C07X16/10, C07X19/00, C12N5/10, C12P21/02, PC C12R1:91),
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PC C12R1:91,
CC Description of Artificial Sequence: CD4-scFv(17b) FH Key 1 (bases 1 to 1440) Berger, B.A. and Castillo, C.D. Novel chimeric protein for prevention and treatment synthetic construct synthetic construct artificial sequences. JP 2002538814-A/1. infection Novel chimeric protein infection. source 16-MAR-2000 JP 2000605633 16-MAR-1999 US 60/124681 EDWARD A BERGER, CHRISTIE DEL CASTILLO C12N15/09, A61K38/00, A61P31/18, C07K5/103, C07K14/00, C07K14/155, C07K14/73, C07K16/10, C07K19/00, C12N5/10, C12P21/02//(C12P21/02, Location/Qualifiers /organism='Artificial Sequence' Location/Qualifiers /organism="synthetic construct" /mol_type="genomic DNA" /db_xref="taxon:32630" GI:33078649 1440 for pr 40 bp DNI prevention DNA A linear PAT 17-JUL-2003 and treatment of HIV of HIV 읶

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                        ACAGTCTACCTGGAGCTGCGGAATCTAAGATCTGACGATACGGCCGTATATTTCTGTGCG
                                                          GCACACTACGCACCGCACCTCCAGGGCAGAGTCACGATTACCGCGGACAAGTCCACGAGC
                                                                                           CGACAGGCCCCTGGACAAGGCCTTGAGTGGATGGGAAGGATCATCACTATCCTTGATGTA
                                                                                                                            GTGAAGGTCTCCTGCAAGGCCTCTGGAGACACCTTCATCAGATATAGTTTTTACCTGGGTG
                                                                                                                                                              GGTGGATCCGGTGGCGGAGGGTCGGGGGGTGGAAGCCGGGGGTGGCGCTCCCGAGGC
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TGGTACCAGCAGAAACCTGGCCAGGCTCCCAGGCTCCTCATATATGGGTGCATCCACCAGG
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Sequence 1 from patent US 5223418.
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RA363716
VERSION
RA363716
VERSION
RA363716.1 GI:34425655
SOURCE
Unknown.
Unclassified.
Unclassified.
RATHORS
REFERENCE
ACTUTI, E. J., B.
TITLE
REPLOW LOCALING the yield of heterologous proteins produced by Streptomyces lividans
Streptomyces lividans
FEATURES
BOURCE
JOURNAL
FEATURES
BOURCE
ORIGIN

Query Match

43.4%; Score 625; DB 6; Length 1213;
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RESULT 3
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625; Conservative
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Sequence 30
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Spr identification of inhibitors of receptor-ligand interactions Patent: WO 0122084-A 30 29-MAR-2001;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Jakobsen, B.K.
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GCAGCCACTCAGGGAAAGAAGTGGTGCTGGGCAAAAAAAGGGGATACAGTGGAACTGACC 120
                                                                 ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA
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//db_xref="d1:13619793"
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                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Homo sapiens"
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/db_xref="taxon:9606"
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                                                                                                                                                                                                                                                                 Cocks, Stuart, S.G. and Seilhamer, J. Cocks, B.G., Stuart, S.G. and Seilhamer, J. Compositions for the detection of blood response gene expression patent: US 6607879-A 1013 19-AUG-2003; Location/Qualifiers 1. 1742
                                                                                                                                                                                                                                                                                                                                                                              Unknown.
Unclassified
                                                                                                                                                                                                                                                                                                                                                                                                             Unknown
                                                                                                                                                                       Similarity
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                                                    GCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAAAAAAAGGGGATACAGTGGAACTGACC
                                                                                           ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTTGGTGCTGCAACTGGCGCTCCTCCCA
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                                GCAGCCACTCAGGGAAAGAAGTGGTGCTGGGCAAAAAAAGGGGATACAGTGGAACTGACC
                                                                                                                          ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA
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                                                                                                                                                          Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           1013
                                                                                                                                                                                                                                organism="unknown"
/mol_type="genomic/
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                                                                                                                                                                      43.4%;
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from patent US
                                                                                                                                                         Score 624.4; DB 6;
Pred. No. 1.7e-134;
D; Mismatches 1;
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                                                                                                                                                           625;
                                                                                                                                                                                                                                                                                                                                                                                                        Homo sapiens
Eukaryota; Metazoa; Chordata;
Mammalia; Eutheria; Primates;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AX287109 1742 bp
Sequence 7 from Patent WO0164752
AX287109
                                                                                                                                                                                                                                                                                                              screening methods
Patent: WO 0164752-A 7 07-SEP-2001;
NEW YORK UNIVERSITY (US); KATHOLIE
                                                                                                                                                                        Similarity
                                                                                                                                                                                                                                                                                                                                                          Littman, D.R., Kwon, D., van Kooyk, Y.C. and Geijtenbeek, T.C. Annibody inhibiting the binding between gp120 and dc-sign
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                                                                                                               GTGCTAGCTTTCCAGAAGGCCTCCGG 626
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TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAAACTCCAACCAGATAAAG 180
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                                                                                                                                                           Conservative
                                                                                                                                                                                                                                 /organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"
                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                      43.4%;
                                                                                                                                                       Score 624.4; DB 6;
Pred. No. 1.7e-134;
0; Mismatches 1;
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                                                                                                      T4 is a member of the immunoglobulin supergene family. The T4 mR1 encodes contiguous V- and J-like elements without the requirement for DNA recombination events. The V-like domain can be found at positions 145 to 426 and the J-like domain from 427 to 471. The Typrotein may serve as the specific surface receptor for the AIDS
                                                                                                                                                                                   Unpublished (1986)
Original source text: Human peripheral T lymphocyte, clone pT4B.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Human T-cell surface M12807
                          With the revision of the nucleotide at position encoded by 151-153 becomes lysine. This is now first residue in the mature protein [2].

Location/Qualifiers
                                                                                                                                                                                                                                                                                               The isolation and nucleotide sequence of a cDNA encoding the surface protein T4: a new member of the immunoglobulin gene (Cell 42 (1), 93-104 (1985)
                                                                                                                                                                                                                                                                                                                                                  Axel,R
                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (Dases 1 to 1742)
Maddon,P.J., Littman,D.R., Godfrey,M., Maddon,D.E., Chess,L. and
                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                          antigen; surface antigen.
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glycoprotein; immunoglobulin
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                                                                                             virus [1].
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                                                            153, the amino acid regarded to be the
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                                                                                         GTGCTAGCTTTCCAGAAGGCCTCCGG 626
                                                                                                                                                                                                      AAAAACATACAGGGGGGGAAGACCCTCTCCCGTGTCTCAGGCTGGAGCTCCAGGATAGTGGC
                                                                                                                                                                                                                                               CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT
                                                                                                                                                                                                                                                                    CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT
                                                                                                                                                                                                                                                                                                            CTAGTGTTCGGATTGACTGCCAACTCTGACACCCACCTGCTTCAGGGGCAGAGCCTGACC
                                                                                                                                                                                                                                                                                                                                  CTAGTGTTCGGATTGACTGCCAACTCTGACACCCACCTGCTTCAGGGGGCAGAGCCCTGACC
                                                                                                                                                                                                                                                                                                                                                                          ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGTGCAATTG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /protein_id="AAA35572.1"
/db_xref="GI:179142"
/db_xref="GI:179142"
/ranslation="murgyperhillvlolallpaatogkkvvlgkkgdtveltctag
/kranslation="murgyperhillvlolallpaatogkervlikylkie
Oxksiophwksnoikilgongsfltkgfsklwdradsrrslwdognepliikvlkie
DSDTYICEVEDQKEEVQLLVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRG
RNIQGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLRPGKASSIVYKKEGEQ
VEPSFPLAFTVEKLTGSGELMWQAERASSSKWITFDLKNKEVSVKRVTQDPKLQMGK
KLPLHLTLPQALPQYAGSGNLTLALEAKTGKLHQEVNLVVMRATQLQKNLTCEVWGPT
SPKLMLSIKLENKEAKVSKREKAVWLLNPEAGMWQCLLSDSGQVLLESNIKVLPTWST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="T4 surface glycoprotein signal peptide"
151. .1449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FQKTCSPI"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PVQPMALIVLGGVAGLLLFIGLGIFFCVRCRHRRRQAERMSQIKRLLSEKKTCQCPHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  product="T4 surface glycoprotein mature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /db_xref="taxon:9606"
76._.1452
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Pred. No. 1.7e-134;
                                                            701
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MEDLINE
PUBMED
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91216786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Submitted (12-JUN-1990) T.W. Hodge, A-25 Bldg. 1, for Disease Control, 1600 Clifton Rd. Atlanta, GA Original source text: Human DNA.

A cytosine to thymidine transition at nucleotide presults in substitution of TRP-240 for ARG-240.

Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.

1 (bases 1 to 1742)

Hodge, T.W., Sasso, D.R. and McDougal, J.S.

Humans with OKT4-epitope deficiency have a single nucleotide base change in the CD4 gene, resulting in substitution of TRP240 for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          2 (bases 1 to 1742)
Hodge, T.W.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           glycoprotein; immunoglobulin antigen; surface antigen. Homo sapiens (human)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             HUMATCT4A 1742 bp
Human T4 surface glycoprotein CD4
M35160
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                                                                                                                                                                                                                            Similarity
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  TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCAACCAGATAAAG
                                                                   GCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAAAAAAAGGGGGATACAGTGGAACTGACC
                                          GCAGCCACTCAGGGAAAGAAGTGGTGCTGGGCAAAAAAAGGGGGATACAGTGGAACTGACC
                                                                                                                        ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA
                                                                                                                                                              ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA
                                                                                                                                                                                                       43.4%;
llarity 99.8%;
Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTAS
GKKS10PHKKNSNQIKILGNGSFLTKGPSKLNDRADSRRSLNDGGNFPLIIKNLKE
DSDTYICGNEDQKEFVGLVFGCTANSDTHLLQCGSLTUTLESPPGSSPSVQCRSPRE
ENSTYICGNEDQKEFVGLVFGCTANSDTHLLQCGSLTUTLESPPGSSPSVQCRSPRE
KN1QGGKTLSVSQLELQDSGTWTCTVLQNQKKVEFKIDIVVLAFQKASSIVYKKEGBQ
VEFSFFLAFTVEKLTGSGELMWQAERASSSKSWITPDLKNKEVSYKWYTQDFKLQMGK
KLPLHITLPQALPQYAGSGNLTLALEAKTGKKLQEVNLVWRATQLQKNLTCEVWGFT
SPKLMLSLKLBNKEAKVSKREKAVWYLNFEAGMWQCLLSDSGQVLLLSSNIKTLFWGFT
SPKLMLSLKLBNKEAKVSKREKAVWYLNFEAGMWQCLLSDSGQVLLLSSNIKTLFWGFT
SPKLMLSLKLBNKEAKVSKREKAVWYLNFEAGMWQCLLSDSGQVLLSSNIKTLFCCCPHR
PQQMALI_ULGGVAGLLLFIGLGIFFCVRCRHRRRQAERMSQIKRLLSEKKTCQCPHR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /gene="CD4"
76. .1452
                                                                                                                                                                                                                                                                                                                                                                                                            /gene="CD4"
/note="T4 surface glycoprotein signal peptide"
151. .1449
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /mol_type="unassigned DNA"
/db_xref="taxon:9606"
/haplotype="OKT4-negative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /codon_start=1
/protein_id="AAA16069.1"
/db_xref="GI:179144"
                                                                                                                                                                                                                                                                                                        'gene="CD4"
'note="g in
                                                                                                                                                                                                                                                                                                                                                                                      gene="CD4"
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                                                                                                                                                                                                                                                                                                                                                                   product="T4 surface glycoprotein
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                                                                                                                                                                                                                                                                                                          in OKT4 epitope deficiency; c
                                                                                                                                                                                                       Score 624.4; DB 9;
Pred. No. 1.7e-134;
); Mismatches 1;
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30333 USA
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                                                                                                                                                                                                                                      Cloned genes encoding IG-CD4 fusion proteins Patent: EP 0325262-A2 3 26-JUL-1989;
Location/Qualifiers
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Brian, S.D.
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Sequence 3 from
108116
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                                                                                                                                                                                                                                                                                              Unclassified.
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                                                                                                                                                              Similarity
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                                                               GCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAAAAAAAGGGGATACAGTGGAACTGACC
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/mol_type="unassigned
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Sequence
108115
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Brian, S.D.
Cloned genes encoding IG-CD4 fusion proteins
Patent: EP 0325262-A2 1 26-JUL-1989;
Location/Qualifiers
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 GACTCAAGAAGCCTTTGGGACCAAGGAAACTTCCCCCCTGATCAAGAATCTTAAG
                                    TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCAACCAGATAAAG
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/mol_type="unassigned
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A baculovirus expression system for magnetic cells and enhanced titer determination
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (16-OCT-2003) LDC / Basel CH-4002, Switzerland
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AY438650
AY438650.1 GI:38197734
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Philipps, B., Forstner, M.
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1 (bases 1 to 7533)
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Best Local Similarity
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VTAAGITLGMDELYK"
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Pred. No. 1.7e-134;
0; Mismatches 1;
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REFERENCE
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Best Local Similarity 99.7%;
Matches 624; Conservative
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Sequence
106223
106223.1
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Deen,K.C., Folena-Wasserman,G.M., Inacker,R.
Process for purification of soluble T4
Patent: EP 0313377-A1 1 26-APR-1989;
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Unknown.
Unclassified.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           organism="unknown"
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Pred. No. 4.1e-134;
0; Mismatches 2;
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EP 0313377.
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Arthos, J., Clark, P.E., Fornwald, J.A., Brawner, M.E., Gorman, J.A., Sathe, G.M., Sweet, R.W. and Taylor, D.P. Expression of HIV binding proteins Expression of HIV binding proteins Patent: EP 0331356-A2 1 06-SEP-1989;
Location/Qualifiers
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 GTGCTAGCTTTCCAGAAGGCCTCCAG
                                                     ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
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E 1 (bases 1 to 1304)

S Seed, B., Banapour, B., Romeo, C. and Kolan Targeted cytolysis of HIV-infected cells receptor-bearing cells receptor-bearing cells Location/Qualifiers

1 1304 """known" nam"
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GTGCTAGCTTTCCAGAAGGCCTCCGG
                                         ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
                                                                                             AAAAACATACAGGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC
                                                                                                                                      CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT
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                                                                       GTGCTAGCTTTCCAGAAGGCCTCCGG
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1 (bases 1 to 1389)
Seed, B., Romeo, C. and Kolanus, W. Redirection of cellular immunity by Patent: US 5843728-A 2 01-DEC-1998; Location/Qualifiers
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                                                                                            ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
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Aaa50662 DNA encod
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Aaa35205 Human ade
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1728	1727	1599	1599	1599	1599	1389	1389	1389	1389	1389	1304	1304	6019	6019	6019	6019	3133	3133	3133	3133	2589	2589	2589
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DNA enc	Aaq96124 T-cell re	Aav70157 Chimeric	Aat36760 CD4:T-cel	Aat10803 CD4:eta f	Aag28706 DNA encod	Aav70158 Chimeric	_	Aat10802 CD4:gamma	Aaq96123 T-cell re	Aaq28705 DNA encod		Aaq96103 CD4 domai	Abd20873 Human pul	Abz97024 Human nuc	Aaf21330 Human low	Aaa35208 Human ade	Aaz48201 DNA seque	Aaz44061 Human fus	Aaa50660 DNA encod	Aan90356 Genetic c	Aaz48202 DNA seque	Aaz44062 Human fus	Aaa50661 DNA encod

ALIGNMENTS

RESULT 1 AAA54045 Fusion protein; HIV; human immunodeficiency virus; antibody; Fv; AIDS; acquired immune deficiency syndrome; neutralisation; infection; gene therapy; CD4; gpl20; glycoprotein; resistance; vaccination; binding domain; single chain antibody; chimera; chimeric protein; ds. Synthetic. Human immunodeficiency virus. 08-FEB-2001 (first entry) AAA54045; AAA54045 standard; DNA; 1440 BP WO200055207-A1 sCD4-SCFv(17b) HIV single chain antibody fusion protein. /*tag= a /product= "CD4-SCFV(17b) fusion protein." /product= "This sequence does not fully encode the cross referenced protein given in GENESEQ record AAB00158. ?protein sequence also comprises a 28 amino acid Cterminal peptide" Cocation/Qualifiers That

21-SEP-2000.

16-MAR-1999;

99US-0124681P.

16-MAR-2000; 2000WO-US006946.

Novel neutralizing bispecific fusion proteins effective in viral such HIV neutralization, comprises two different binding domains, inducing-

as

WPI; 2000-638183/61. P-PSDB; AAB00158.

Berger EA, Del Castillo CM;

(USSH) US NAT INST OF HEALTH

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SCD4-SCFv(17b) is a neutralising bispecific fusion protein capable of CC binding to two sites of its target protein. The protein comprises a first CC binding domain capable of binding domain side on the target protein, a second binding domain capable of forming neutralising complex CC with an induced epitope of the target protein and a linker connecting the CC contealing domains. SCD4-SCFv(17b) comprises a soluble CD4 fragment CC (contealing domains D1 and D2) fused to a single chain Fv portion of CC mimetic is used for inactivating 9p120 protein of HIV, and for CC neutralising HIV. It is also used for blocking and preventing the binding CC fit he viral or recombinant 9p120 protein to soluble CD4 or lymphocyte CC D4 and for inhibiting HIV replication. The chimeric proteins is CC therefore useful for treating HIV infection and also AIDS. It is are particularly useful in the prevention of infection during or immediately after HIV exposure (e.g., mother/infant transmission, post-exposure CC resistance to HIV infections and AIDS. Gene therapy is used to secrete CC the bispecific protein at mucosal surfaces, such as the vaginal, rectal CC reactive with neutralising antibody with high in vivo activity and no Fc-mediated undesirable targetting properties. When the fusion protein is CC substentially derived from human proteins. When the fusion protein is CC and toxicity in humans which is of great value in prevention of infection of
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                                                                                                                 vector DNA
                                                                      complex; gp120; CD4; HIV; HIV infection; anti-HIV; circular;
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11-MAY-1998;
07-JAN-2000;
                                                                                                                                                                                                                                                                                                                                                                                              The invention relates to an immunogenic complex comprising gp120 covalently bonded to a CD4 equivalent molecule, fragment of CD4 or its equivalent. The invention also relates to a composition comprising the complex and a carrier, an antibody reactive with the complex, an immortalised cell line that produces the complex, a method of detecting the HIV antigen in a test fluid, involving contacting the test fluid with an antibody raised against the immunogenic complex and detecting the presence of immune complexes formed between the antigen in the test fluid and the antibody, and a vaccine comprising an immunogenically effective amount of the immunogenic complex. The immunogenic complex is useful for raising neutralising antibodies against HIV, which involves administering the complex to a subject in a carrier, and for treating HIV infections. This sequence represents expression vector DNA used in the scope of the
                                                                                                                                                                                                                                                                                                                                                             Sequence 8911 BP;
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ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGAGGTGCAATTG
                                       GACTCAAGAAGCCTTTGGGACCAAGGAAACTTCCCCCTGATCATCAAGAATCTTAAG
                                                             GACTCAAGAAGAAGCCTTTGGGACCAAGGAAACTTCCCCCTGATCATCAAGAATCTTAAG
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94WO-US005020.
95US-00464680.
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                                               Sequential screening of candidate compounds library for those which inhibit binding of low affinity receptor-ligand interaction having binding kinetics, using interfacial optical assay.
                                                                                                                                                                                                                                                              mat_peptide
                                                                                                                                                                                                                                                                                                                                                                             Human; CD4; T4; CD4 fusion protein; oligomerisation; receptor-ligand interaction inhibition; surface plasmon resonance; T cell receptor binding; MHC binding; carcinoma; autoimmune disease multiple sclerosis; human immunodeficiency virus; HIV; diabetes;
                                                                                           P-PSDB;
                                                                                                                                                                   21-SEP-1999;
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present sequence encodes human CD4.

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CD4 oligomerisation

Human CD4 extracellular domains

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   25-MAR-2003
                                   AAQ38761;
                                                                   AAQ38761 standard; DNA; 1415
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
                                                                                                                                                                      GTGCTAGCTTTCCAGAAGGCCTCCGG 626
                                                                                                                                                                                                                                   ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
                                                                                                                                                                                                                                                                                                   AAAAACATACAGGGGGGGGAAGACCCTCTCCGTGTCTCAGCCTGGAGCTCCAGGATAGTGGC
                                                                                                                                                                                                                                                                                                                                                                  CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT
                                                                                                                                                                                                                                                                                                                                                                                                                CTAGTGTTCGGATTGACTGCCAACTCTGACACCCACCTGCTTCAGGGGCAGAGCCTGACC
                                                                                                                                                                                                                                                                                                                                                                                                                                   CTAGTGTTCGGATTGACTGCCAACTCTGACACCCCACCTGCTTCAGGGGCAGAGCCTGACC
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                                                                                                                                                                                                                                                                                  AAAAACATACAGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCAACCAGATAAAG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCAACCAGATAAAG
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   (revised)
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Pred. No. 1.6e-129;
                                                                   ₽P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          C; 393 G; 278 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
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Matches
                                                                                                                                                                                           Query Match
                                                                                                                                                                                                                            New fusion protein used in gene therapy for treating AIDS - compuprotein which binds to retroviral envelope protein which targets protein to lysosome.
                                                                                                                                                                                                             Sequence 1415 BP; 360 A;
                                                                                                                                                                                                                                                                                                              Claim 12; Page 14-15; 47pp; English.
                                                                                                                                                                                                                                                                                                                                                                     WPI; 1993-117537/14.
                                                                                                                                                                                                                                                                                                                                                                                                                           26-SEP-1991;
                                                                                                                                                                                                                                                                                                                                                                                                                                             22-SEP-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-APR-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  misc_feature
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    polymerase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sCD4-L2 lysosomal targeting fusion gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                22-JUL-1993
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WO9306216-A1
                                                                                                                                                                                                                                                                                                                                                                                                         (OKLA-) OKLAHOMA MED
                                                                                                                                                                                  Local
          241
                                             181
                                                               201
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                            261
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                                                                                                                                                                           625;
                                                                                                                      61
                                                                                                                                        81
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CD4; HIV; Human immunodeficiency Virus; envelope; glycoprotein; ase chain reaction; lysosomal membrane protein; lamp-2; ss.
                                                                                                                                                                                  Similarity
GACTCAAGAAGAAGCCTTTGGGACCAAGGAAACTTCCCCCTGATCATCAAGAATCTTAAG
                                                                          TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCCAACCAGATAAAG
                                                                                                              GCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAAAAAAAGGGGATACAGTGGAACTGACC
                                                                                                                                                  ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA
                                         GCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAAAAAAAGGGGGATACAGTGGAACTGACC
                                                                                                                                         ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA
                            TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAAACTCCAACCAGATAAAG
                                                                                                                                                                         43.4%;
ilarity 99.8%;
Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (first
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                                                                                                                                                                                                                                                                                                                                                                                                                                             92WO-US008090
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/note= "xbal restriction site"
1410 . 1415
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1275. .
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                                                                                                                                                                                                              365 C;
                                                                                                                                                                           0,
                                                                                                                                                                                 Score 624.4;
Pred. No. 1.6
                                                                                                                                                                                                              393 G;
                                                                                                                                                                           Mismatches
                                                                                                                                                                                  1.6e-129;
                                                                                                                                                                                                              297 T; 0 U; 0 Other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      site"
                                                                                                                                                                                             DB
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A
Claim 5; Page 31-33; 43pp;
                                                                                  Composition for treating or preventing human immune deficiency virus, comprises CD4 chimeric protein having a protective effect in trans, or
                                                                                                                                                                                                  WPI; 2003-779059/73
                                                                                                                                                                                                                                                    Alarcon Sanche
Gomez Buendia
                                                                                                                                                                                                                                                                                                                                                                                                 14-MAR-2002; 2002ES-00000616
                                                                                                                                                                                                                                                                                                                                                                                                                                                      14-MAR-2003; 2003WO-ES000120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           endoplasmic reticulum; ER retention; envelope protein
T cell receptor CD3epsilon chain; C-terminal domain; (
gene therapy; human; gene; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HIV-1 infection; human immunodeficiency virus-1; CD4+ cell; chimeric
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CD4/TCR CD3epsilon chain chimeric protein CD4epsilon15 DNA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   04-DEC-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADA44806
                                                     related nucleic acid
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                                                                                                                                                                                                                                                                                                                                         (CNSJ)
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                                                                                                                                                                                                                                                       Sanchez
uendia M;
                                                                                                                                                                       ADA44807.
                                                                                                                                                                                                                                                                                                                                         CONSEJO SUPERIOR INVESTIGACIONES CIENTIF.
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/partial
/product= "CD4epsilon15"
/note= "No stop codon given"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
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                                                                                                                                                                                                                                                                                    Martinez
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                                                                                                                                                                                                                                                                                    Notario
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CD4epsilon15;
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resulting in HIV-1 retention in the ER and thereby preventing viral replication. In a specific embodiment, the chimeric CD4 molecule comprises CD4 fused to 15 amino acids of the C-terminal domain of the T cell receptor CD3epsilon chain; this chimeric CD4 molecule is designated CD4epsilon15 (ADA44807). A known chimeric CD4 of similar structure but containing only 10 amino acids from CD3epsilon can also be used. Compositions of the invention have an in trans effect on the replication of HIV-1, and may be used to treat and prevent HIV-1 infection. The present sequence represents a DNA encoding the chimeric CD4 molecule CD4epsilon15, which is specifically claimed for use in compositions of
                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a composition for the treatment or prevention of human immunodeficiency virus-1 (HIV-1) infection. The composition comprises CD4+ cells that have been transduced with a vector that encodes a chimeric CD4 molecule which is capable of being retained in the endoplasmic reticulum (ER). The invention also encompasses the use of a soluble protein factor produced by CD4+ cells that have been transduced with a vector encoding a chimeric CD4 protein; and the use of an expression system encoding a chimeric CD4 protein. The ER-localised chimeric CD4 molecule binds to the HIV-1 envelope protein gp160,
                                                            invention.
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Sequence 1419 BP; 362 A; 367 C; 405 G; 285 T, 0 Ç 0 Other;

Similarity

43.48;

DB 10;

Length 1419;

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                   GTGCTAGCTTTCCAGAAGGCCTCCGG
                                                                                       ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGTGGAGTTCAAAATAGACATCGTG
                                                                                                                                                                                                                          CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT
                                                                                                                                                                                                                                                                                          CTAGTGTTCGGATTGACTGCCAACTCTGACACCCACCTGCTTCAGGGGCAGAGCCTGACC
                                                                                                                                                                                                                                                                                                                                                                                                           GACTCAAGAAGCCTTTGGGACCAAGGAAACTTCCCCCTGATCATCAAGAATCTTAAG
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GTGCTAGCTTTCCAGAAGGCCTCCAG
                                                                  ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
                                                                                                                                                                  AAAAACATACAGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC
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Pred. No. 1.6e-129;
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                                                                                                                                                                                                                                                                                                                                                         New fusion protein used in gene therapy for treating AIDS - comprises protein which binds to retroviral envelope protein which targets fusion protein to lysosome.
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22-JUL-1993
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                                                                                                                                                                                                                                                                                                                        Sequence 1421 BP; 355 A; 382 C; 401 G; 283 T;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 12; Page 13-14; 47pp; English.
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                                                                                 GCAGCCACTCAGGGAAAGAAGTGGTGCTGGGCAAAAAAAGGGGGATACAGTGGAACTGACC
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llarity 99.8%;
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/note= "EcoRI restriction
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fusion protein used in gene therapy for treating AIDS

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RESULT 8
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                09-JAN-2001
                                                                     AAA50662
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1448 BP; 357 A; 395 C; 404 G; 292 T; 0 U; 0 Other;
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Pred. No. 1.6
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ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA

ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA

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Query Match
Best Local S
Matches 625
                                                                    The present sequence is that of DNA encoding fusion protein CD4Mmu (see AAB19509) comprising the extracellular portion of CD4, which binds to HIV gp120, linked at its C-terminus to a human IgM heavy chain polypeptide. To obtain the construct, DNA encoding CD4 was linked to IgM DNA at the Mst2 site upstream of the CH1 region. A plasmid containing this genetic construct is deposited in Escherichia coli MC1061/P3 as ATCC 67809. Fusion protein CD4Mmu and a nucleic acid encoding it are claimed. Also claimed are a vector comprising the nucleic acid, and a method of producing the fusion protein may further comprise a therapeutic agent, radiolabel or NMR inaging agent. The fusion protein can be administered to an animal (including humans) for treatment of HIV or SIV infection, and can also be used in assays for HIV or SIV, imaging and tissue stains. IgM fusion proteins such as CD4Mmu provide complement-mediated immunity
                                                                                                                                                                                                                                                                                                                                                                                                           22-JAN-1988;
23-JAN-1989;
09-JUN-1992;
12-APR-1993;
04-FEB-1994;
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P-PSDB; AAB19509.
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  al Similarity 625; Conserv
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 43.4%; ilarity 99.8%; Conservative
                                                BP;
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89US-00299596.

92US-00896781.

93US-00057952.

94US-00191708.
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23-JAN-1989;
09-JUN-1992;
12-APR-1993;
   WPI; 2000-085792/07.
P-PSDB; AAY51080.
                                                                                                                                                                                                                                                                                                                                                                               Fusion protein; human; CD4; IgM; immunoglobulin; gp120; anti-human immunodeficiency virus; CD4Mg; ds.
                                                       Seed B;
                                                                                                                                                                                                                     04-FEB-1994;
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89US-00299596.
92US-00896781.
93US-00057952.
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Best Local Similarity
                                                                          AAZ48203
       14-MAR-2000
                                        AAZ48203;
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Fusion
                        protein useful
  S
  41-50;
                          for the treatment
39pp; English
                          of human
                          immunodeficiency virus.
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This invention describes a novel nucleic acid (I) encoding a fusion protein comprising a DNA sequence encoding amino acids 1-173 of CD4 (II) and a DNA sequence encoding a mino acids 1-18 heavy or light chain (III). The products pf the invention have anti-human immunodeficiency virus (HIV) activity and are capable of binding to gp120. The fusion protein is useful for treating human immunodeficiency virus (HIV) or simian immunodeficiency virus (SIV). This sequence encodes the fusion protein CD4Mg which is constructed from CD4 linked to human the fusion protein CD4Mg which is constructed from CD4 linked to human IGM upstream of the CH1 region

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Sequence 1714 BP; 411 A; 503 C; 467 G;
      333 T; 0 U; 0 Other;
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DB u -

Length

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Matches
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                                ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAAAAAAAGGGGATACAGTGGAACTGACC
                                                                                                                                                                             CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT
                                                                                                                                                                                                                                        CTAGTGTTCGGATTGACTGCCAACTCTGACACCCACCTGCTTCAGGGGCAGAGCCTGACC
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 GTGCTAGCTTTCCAGAAGGCCTCCGG
                                                                                              AAAAACATACAGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC
                                                                                                                             ANAAACATACAGGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC
                                                                                                                                                            CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCTCAGTGCAATGTAGGAGTCCAAGGGG
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; Pred. No. 1.6e
0; Mismatches
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711

GTGCTAGCTTTCCAGAAGGCCTCCAG

standard;

DNA; 1714

ВP

(first entry)

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Query Match
Best Local (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The invention provides a fusion gene encoding a fusion protein that comprises an extracellular CD4 DNA sequence or its fragment which binds to HIV gp120 when fused to an immunoglobulin (Ig) chain and the DNA sequence of an Ig heavy or light chain, where the DNA sequence encoding the variable region has been replaced with the DNA sequence which encodes extracellular CD4 or its gp120 binding fragment. The fusion protein is capable of being secreted. The fusion proteins are useful for treating HIV or SIV infections in animals, preferably humans. They are also useful infections in humans. The present sequence represents the DNA which encodes the fusion protein CD4Mmu where the CD4 is linked to human IgG1 at the Mst2 site upstream of the CH1 region
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 1714 BP; 411 A; 503 C; 467 G;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           fusion gene encoding immunoglobulin-CD4 fusion proteins, useful treatment of HIV or simian immunodeficiency virus infections.
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DB; AAY59170.
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CTAGTGTTCGGATTGACTGCCAACTCTGACACCCCACCTGCTTCAGGGGCAGAGCCTGACC
                                        ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGTGCAATTG
                                                                 ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGAGGTGCAATTG
                                                                                                                            GACTCAAGAAGCCTTTGGGACCAAGGAAACTTCCCCCCTGATCATCAAGAATCTTAAG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Score 624.4;
Pred. No. 1.6
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                                              The present invention describes a new composition comprising an antise oligonucleotide (ON) with low adenosine (up to 15%), which targets nucleic acids involved in bronchoconstriction, allergies, and/or inflammation. The ON can have antiinflammatory, antiallergic, antiasthmatic, cytostatic and analgesic activities. The compositions a useful for the treatment of diseases associated with inflammation, impaired airways, including lung disease and diseases whose secondary effects afflict the lungs of a subject. They can be used for treating the first the lungs of a subject. They can be used for treating
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Human, adenosine receptor, low adenosine antisense oligonucleotide; phosphorothicate; impaired respiration; inflammation; allergy; phosphorothicate; impaired respiration; infibitor; antiinflammatory; allergic disease; bronchoconstriction; inhibitor; antiinflammatory; lambilergic; antiasthmatic; cytostatic; analgesic; impaired airway; lung disease; ischaemic condition; pulmonary vasoconstriction; asthm respiratory distress syndrome; pain; cystic fibrosis; emphysema; pulmonary hypertension; chronic obstructive pulmonary disease; COPD;
                                                                                                                                                                                                                                                                New antisense oligonucleotides useful for treating e.g. pulmonary vasoconstruction, inflammation, allergies, asthma, hypertension, bronchitis, emphysema, respiratory distress syndrome, ischemia ox
                                                                                                                                                                                                                Disclosure;
                                                                                                                                                                                                                                                                                                                                           WPI; 2000-205971/18.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      03-AUG-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Human adenosine receptor related polynucleotide 2nd SEQ ID NO:79.
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                                                                                                                                                                                                                                                                                                                                                                                                               (UYEC-) UNIV EAST CAROLINA
                e.g. ischaemic conditions, pulmonary vasoconstriction, allergies, mpeded respiration, respiratory distress syndrome, pain, cystic
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pulmonary hypertension,
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Query Match
Best Local Similarity
Matches 625; Conserv
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14-MAR-2001
                                                                                                AAF21327 standard; DNA; 1742
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(first entry)
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Pred. No. 1.6e-129;
0; Mismatches 1;
                                                                                                   ВP
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Human low adenosine antisense oligonucleotide related sequence #2894.
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Low adenosine antisense oligonucleotide; phosphorothioate; allergy; human; airway disorder; bronchoconstriction; lung inflammation; surfactant depletion; respiratory; bronchodilator; antiinflammattory; immunosuppressive; antiasthmatic; analgesic; hypotensive; cytostatic; respiratory obstruction; pulmonary obstruction; impeded respiration; surfactant hypoproduction; pulmonary vasoconstriction; asthma; RDS; respiratory distress syndrome; pain; cystic fibrosis; allergic rhinitis; pulmonary distress syndrome; pain; cystic fibrosis; allergic rhinitis; chronic obstructive pulmonary disease; pulmonary infection; bronchitis; cancer; ss.

Homo sapiens.

WO200062736-A2.

26-OCT-2000.

24-MAR-2000; 2000WO-US008020 06-APR-1999; 99US-0127958P

(UYEC-) UNIV EAST CAROLINA. (NYCE/) NYCE J W.

Nyce JW;

WPI; 2000-679539/66.

Low adenosine (A) content antisense oligonucleotides which do not trigger adenosine receptors during metabolism, useful e.g. for treating cancers and respiratory obstructions.

Disclosure; Page 1329; 1592pp; English.

The present invention describes low adenosine (A) content antisense coligonucleotides and compositions (I) comprising them. In the antisense (C) coligonucleotides the A is replaced by a 'Universal' or alternative base. (C) can have respiratory, bronchodilator, antiinflammatory, analgesic, cimmunosuppressive, antiasthmatic, hypotensive and cytostatic activities. The antisense oligonucleotides and (I) can be used to down-regulate the compression and or activity of target polypeptides associated with coling/respiratory disorders and malignancies, such as stimulating and cativating peptide factors and transmitters, transcription factors, immunoglobulins and antibodies, antibody receptors, cytokines and chemokines, endogenously produced specific and non-specific enzymes, binding proteins, adenosine receptors, bradykinin receptors, cytokine and creceptors, cytokine and cytostation, receptors, cytokine and creceptors, cytokine and cytostation, cytokine and cytostation receptors, cytokine and cytostation and peripheral nervous and non-nervous system peptide receptors, cytokine and cytostation, cytokine and cytostation creceptors, cytokine and cytostation and malignancy associated proteins. The antisense oligonucleotides may be used in this way to treat disorders and cytostation, cytokine and cytostation, pub

Sequence 1742 BP; 405 A; 492 C; 466 G; 379 T; 0 U; 0 Other;

Query Match 43.4%; Score 624.4; DB 3; Length 1742; Best Local Similarity 99.8%; Pred. No. 1.6e-129; Matches 625; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

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                                                                                                 07-SEP-2001
                                                                                                                                                       C-type
                                                                                                                                                                                    Nucleotide sequence of a human polynucleotide.
                                                                                                                                                                                                         10-DEC-2001
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                                                                                                                                                       receptor; DC-SIGN; dendritic cell; T lymphocyte; HIV; gp120; lectin; ICAM3; HIV entry; T cell; macrophage; HIV infection;
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An antibody for the treatment or prevention of HIV-infection comprises gp120 portion which binds to DC-SIGN or is exposed upon gp120 binding of DC-SIGN due to concomitant conformational change. WPI; 2001-602565/68 Of a

Disclosure; Page 121-122; 131pp; English.

The specification describes an antibody which is specific for an antigenic fragment of gpl20. This antigenic fragment binds to DC-SIGN or is exposed upon gpl20 binding of DC-SIGN due to concomitant conformational change. DC-SIGN is a receptor that is specifically expressed on dendritic cells and facilitates infection of T lymphocytes with HIV. DC-SIGN is identical to a HIV-1 gpl20-binding C-type lectin. I -SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes) with high affinity. The antibody of the invention inhibits the trans enhancement of HIV entry into a T cell or macrophage facilitated by dendritic cells. The antibody is useful to treat or prevent HIV infection. The present sequence represents a human polynucleotide, which is used in the course of the invention which ç g

Sequence 1742 BP; 405 A; 491 C; 466 G; 380 T; 0 U; 0 Other;

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Score 624.4; DB 4; Pred. No. 1.6e-129; 0; Mismatches 1;

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                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel pharmaceutical composition, which has a CC first active agent comprising an oligonucleotide antisense to the CC initiation codon, coding region, 5' or 3' end genomic flanking regions, CC 5' and 3' intron-exon junctions, or regions within 2-10 nucleotides of junctions of genes encoding a polypeptide associated with lung and/or CC nasal airway dysfunction and a second active agent comprising an CC antiinflammatory steroid and ubsquinone. A composition of the invention CC immunosuppressive, and cytostatic activity. The composition may have a CC immunosuppressive, and cytostatic activity. The composition may have a CC immunosuppressive, and cytostatic activity. The composition may have a CC immunosuppressive, and cytostatic activity. The composition may have a CC or enhancing the prophylactic or malignant disease or condition, also CC for enhancing the prophylactic or therapeutic respiratory effect of an antiinflammatory steroid in a subject, for reducing or depleting levels of adenosine CC for reducing sensitivity to adenosine, reducing levels of adenosine conceptor, producing bronchodilation, increasing levels of ubiquinone or CC lung surfactant in a subject's tissue, or treating bronchoconstriction, CC lung inflammation, lung allergies, or a respiratory disease or condition. CC Note: The sequence data for this patent is not represented in the printed car firm, who distance on the prophylactic or the sequence or condition.
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Miller S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Pharmaceutical composition for treating ailments associated with impaired respiration, has oligo(s) antisense to specific gene(s) or its corresponding RNAs, and glucocorticoid or non-glucocorticoid steroid or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Human; antisense; lung dysfunction; nasal airway dysfunction; antiinflammatory steroid; ubiquinone; antiinflammatory; antiallergic; antiasthmatic; hypotensive; immunosuppressive; cytostatic; gene therapy antisense gene therapy; respiratory; lung; adenosine sensitivity; adenosine receptor; bronchodilation; bronchoconstriction; lung allergy;
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Crohn's disease; asthma; ulcerative colltis; hypereosinophilia;
irritable bowel syndrome; osteoarthritis; rheumatoid arthritis;
acute monocytic leukaemia; antiinflammatory; antiasthmatic; ant
osteopathic; antiarthritic; antirheumatic; cytostatic.
A composition comprising a plurality of cDNAs, useful for detecting altered expression of genes in an immunological response or for % \left( 1\right) =\left\{ 1\right\} 
                                                    WPI; 2003-895307/82.
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The invention relates to a composition comprising a plurality of cDNAs CC for detecting the altered expression of genes in an immunological CC response. The invention also relates to a method of diagnosing or comprising the treatment of an immunopathological condition in a sample, CC monitoring the treatment of an immunopathological condition in a sample, comparising obtaining nucleic acids from a sample, contacting the nucleic comparising of the sample with an array comprising the plurality of cDNAs under comprising the plurality of cDNAs under conditions to form one or more hybridisation complexes, detecting the conditions of the sample, where an altered level of the detected hybridisation complexes with the level of hybridisation complexes correlates with the presence of an immunopathological condition. Also disclosed are an expression profile comprising a microarray and a plurality of detectable complexes and a comprising a microarray and a plurality of polynucleotide probes. The cDNAs concentration immunopathology, such as Crohn's disease. The microarray can be used in the diagnosis of an immunopathology, such as Crohn's disease, asthma, concentrative colitis, hypereosinophilia, irritable bowel syndrome, consecutiving agents for the treatment of the diseases. The microarray may console used in drug discovery and development, toxicological and consecutive consecutive studies, forensics or pharmacogenomics. The composition carcinogenicity studies, forensics or pharmacogenomics. The composition convergence had a bundan cDNA of the printed specification but was obtained in electronic format directly convergence had a suppose that directly are printed as a user of convergence had a suppose that directly convergence and a suppose that directly are the printed specification but was obtained in electronic format directly convergence and a suppose that direc from USPTO at seqdata.uspto.gov/sequence.html. Claim 1; SEQ ID NO 1013; 50pp; English. diagnosing and treating an immunopathology, e.g. Crohn's disease, asthma or osteoarthritis.

Sequence 1742 BP; 405 A; 491 C; 466 G; 380 T; 0 U; 0 Other;

Query Match Best Local Matches 62	Match 43.4%; Score 624.4; DB 11; Length 1742; Local Similarity 99.8%; Pred. No. 1.6e-129; les 625; Conservative 0; Mismatches 1; Indels 0; Gaps 0;	
ş	1 ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGGGCTCCTCCCA 60	
Db	76 ATGAACCGGGGAGTCCCTTTTAGGCACTTGCTTCTGGTGCTGCAACTGGCGCTCCTCCCA 135	
Ş	61 GCAGCCACTCAGGGAAAGAAAGTGGTGCTGGGCAAAAAAAGGGGATACAGTGGAACTGACC 120	
Db	136 GCAGCCACTCAGGGAAAGAAGTGGTGGTGCTGGGCAAAAAAGGGGGATACAGTGGAACTGACC 195	
Ş	121 TGTACAGCTTCCCAGAAGAAGAAGAACATTCCACTGGAAAAAACTCCAACCAGATAAAG 180	
B	196 TGTACAGCTTCCCAGAAGAAGAGCATACAATTCCACTGGAAAAACTCCAACCAGATAAAG 255	
Ş	181 ATTCTGGGAAATCAGGGCTCCTTCTTAACTAAAGGTCCAATCCAAGCTGAATGATCGCGCT 240	
Вb	256 ATTCTGGGAAATCAGGGCTCCTTCTTAACTAAAGGTCCATCCA	
SA.	241 GACTCAAGAAGACTTTGGGACCAAGGAAACTTCCCCCTGATCATCAAGAATCTTAAG 300	
Вb	316 GACTCAAGAAGCCTTTGGGACCAAGGAAACTTCCCCCTGATCATCAAGAATCTTAAG 375	
Ş	301 ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGAGGTGCAATTG 360	
Db	376 ATAGAAGACTCAGATACTTACATCTGTGAAGTGGAGGACCAGAAGGAGGAGGTGCAATTG 435	
8	361 CTAGTGTTCGGATTGACTGCCAACTCTGACACCCCACCTGCTTCAGGGGCAGAGCCTGACC 420	
Db	436 CTAGTGTTCGGATTGACACTCTGACACCCCACCTGCTTCAGGGGCAGAGCCTGACC 495	
Ş	421 CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT 480	
Ъ	496 CTGACCTTGGAGAGCCCCCCTGGTAGTAGCCCCCTCAGTGCAATGTAGGAGTCCAAGGGGT 555	
Ş	481 AAAAACATACAGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC 540	

	676 GTGCTAGCTTTCCAGAAGGCCTCCAG 701	рь	
	601 GTGCTAGCTTTCCAGAAGGCCTCCGG 626	φ	
41-	616 ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG 675	рь	
4,	541 ACCTGGACATGCACTGTCTTGCAGAACCAGAAGAAGGTGGAGTTCAAAATAGACATCGTG 600	Qy	
.,,	556 AAAAACATACAGGGGGGAAGACCCTCTCCGTGTCTCAGCTGGAGCTCCAGGATAGTGGC 615	<u>В</u>	

Search completed: November 22, 2004, 11:05:33 Job time: 760 secs

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Result
No.
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Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Scoring table:
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length: 2000000000
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Match Length
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*
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1 MNRGVPFRHLLLVLQLALLP......GTRLEIKLVPRGSGHHHHHH
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      DB
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                    US-09-039-555B-15
US-09-517-605-3
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US-08-284-391B-29
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US-08-2457-918-1
US-08-246-368-4
US-08-244-391B-5
US-08-244-391B-5
US-08-244-391B-5
US-08-244-391B-5
US-08-244-391B-6
US-08-2417-495-6
US-08-394-398A-6
PCT-US95-00454-5
PCT-US95-00454-6
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5223394-11
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Compugen Ltd.
  Sequence
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Patent No. 5223394
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  15, Appli 25, Appli 29, Appli 29, Appli 1, Appli 1, Appli 1, Appli 1, Appli 1, Appli 1, Appli 5, Appli 5, Appli 5, Appli 5, Appli 5, Appli 6, Appli
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                                RESULT 2
5223394-11.
5223394-1.
; Patent No. 5223394
; APPLICANT: WALLNER, BARBARA
; TITLE OF INVENTION: RECOMBINANT DNA MOLECULE COMPRISING
; LYMPHOCYTE FUNCTION-ASSOCIATED ANTIGEN 3 PHOSPHATIDYLINOSITOL
; LINKAGE SIGNAL SEQUENCE
; NUMBER OF SEQUENCES: 12
; CURRENT APPLICATION DATA:
; APPLICATION NUMBER: US/07/335,688
; PILING DATE: 10-APR-1989
; SEQ ID NO:11:
; LENGTH: 318 5223394-11
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9 9 9 9 9	Query M Best Lo Matches Oy Db	RESULT 1 5223394-9 PATENT NO. APPLIC ITILE LIVINGHOCYTE LIVINGE SI UNUMEES UUMEEN UUMEEN UUMEEN LIVINGE SI UUMEEN LIVINGE SI UUMEEN LIVINGE SI		44444 300 300 300 300 300 300 300 300 30
61 ILGNQGSFLTKGPSKLNDRADSRRSLMDQGNFFLIIKNLKIEDSDTYICEVEDQKEEVQL	y Match 39.9%; Score 1064; DB 6; Local Similarity 100.0%; Pred. No. 8.3e-54; hes 208; Conservative 0; Mismatches 0; 1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELT	O. 5223394 ICANT: WALLNER, BARBARA E OF INVENTION: RECOMBINANT DNA MOLECULB TE FUNCTION-ASSOCIATED ANTIGEN 3 PHOSPHAT SEIGNAL SEQUENCES: 12 ENT APPLICATION DATA: ENTAPPLICATION UMBER: US/07/335,688 LING DATE: 10-APR-1989 O:9: NGTH: 295	ALIGNMENTS	28 1059 39.7 575 3 US-09-218-950-4 29 1059 39.7 575 4 US-08-394-388A-4 30 1059 39.7 575 5 PCT-US92-0.785-4 31 1059 39.7 575 5 PCT-US95-00454-4 32 1059 39.7 630 4 US-08-472-888A-6 33 1056 39.6 458 6 5223394-7 34 1053 39.5 394 3 US-08-466-368-2 35 1053 39.5 394 3 US-08-328-500-2 36 1051 39.4 530 3 US-08-379-116-4 37 1051 39.4 530 3 US-08-379-116-4 39 1051 39.4 530 3 US-08-379-916-4 40 1051 39.4 530 3 US-08-379-916-4 41 1051 39.4 530 3 US-08-919-14-4 42 1051 39.4 530 3 US-08-919-14-4 43 1051 39.4 530 4 US-09-409-006A-4 44 1050 39.4 530 4 US-09-766-995-4 45 1050 39.4 432 3 US-08-379-516-2
GNFPLIKNLKIEDSDTYICEVEDQKEEVQL 120	Length 295; Indels 0; Gaps 0; CTASOKKSIQFHWKNSNQIK 60	COMPRISING CIDYLINOSITOL		Sequence 4, Appli Sequence 4, Appli Sequence 4, Appli Sequence 6, Appli Sequence 6, Appli Patent NO. 5223394 Sequence 2, Appli Sequence 4, Appli Sequence 2, Appli Sequence 2, Appli Sequence 2, Appli

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Patent No. 603385
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Best Local Similarity
Matches
                                 Query Match
                                                                                                                                                                                                                              COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN Release #1.0, Versic
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/039,555B
FLING DATE: 16-MAR-1998
CLASSIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION UMBER: DE 19710643.9
FILING DATE: 14-MAR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Bent, Stephen A.
REGISTRATION NUMBER: 29,768
REFERENCE/DOCKET NUMBER: 016779/0131
TELECHONE: (202)672-5300
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches 208;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Koerner, Kathrin
APPLICANT: Mueller, Rolf
APPLICANT: Sadlacek, Hans-Harald
TITLE OF INVENTION: PREPARATION AND US
NUMBER OF SEQUENCES: 19
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                    TELEX: 904136
INFORMATION FOR SEQ ID NO:
                                                                                TOPOLOGY: 111
MOLECULE TYPE:
                                                                                                                                                                  SEQUENCE CHARACTERISTICS:
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CITY: Washington
                                                                  -039-555B-15
                                                                                                                   STRANDEDNESS
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               Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
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                                                                                                                                                 LENGTH:
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208;
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                                                                                                                                   amino acid
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                                                                                                                                                                                                                     (202) 672-5399
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 Conservative
                                                                                                   linear
                                                                                protein
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39.9%; Score 1064; DB 3; 100.0%; Pred. No. 1.3e-53; tive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Suite 500
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APPLICANT: Littman, Dan R.
APPLICANT: Kwon, Douglas S.
APPLICANT: wan Kooyk, Yvette
APPLICANT: Geijtenbeck, Tneo
TITLE OF INVENTION: METHODS OF USING A FACILITATOR OF RETROVIRAL ENTRY INTO
TITLE OF INVENTION: CELLS
                                                                                                                                                Sequence 25, Application US/10092138A Patent No. 6743630 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 3, Application US/09517605 Patent No. 6391567
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Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Matches
APPLICANT: Sato, Taka-Aki
TITLE OF INVENTION: METHOD OF PREPARING A PROTEIN ARRAY BASED
TITLE OF INVENTION: BIOCHEMICAL PROTEIN-PROTEIN INTERACTION
FILE REFERENCE: 65823/JPW/PT
CURRENT APPLICATION NUMBER: US/10/092,138A
CURRENT FILING DATE: 2002-03-06
NUMBER OF SEQ ID NOS: 34
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FILE REFERENCE: 1049-1-017
CURRENT APPLICATION NUMBER: US/09/517,605
CURRENT FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
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ORGANISM: Homo
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                                                                                                                                                                                                                                                                                        OPERATING SYSTEM: DOS
SOFTWARE: FRANCED for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/204 CLASSIFT CLASSIFT 02-817
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LENGTH: 458
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Best Local Similarity
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                                                                                                                                                                                     CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
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                INFORMATION FOR SEQ ID NO:
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ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
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APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
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APPLICANT:
SEQUENCE CHARACTERISTICS:
                                                                 FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/247001
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-428-0200
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                                                  TELEFAX: 617-428-7045
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Romeo, Charles
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Pred. No. 1.7e-53;
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; TYPE: amino acid
; STRANDEDNESS: Bingle
; TOPOLOGY: linear
; MOLECULE TYPE: protein
US-08-284-391B-29
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Patent No.
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Best Local Similarity
                                           CLASSIFICATION:

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US/08/284,39:

FILING DATE: 02-AUG-1994

APPLICATION NUMBER: 08/195,395

FILING DATE: 14-FEB-1994

APPLICATION NUMBER: 07/847,566

FILING DATE: 06-MAR-1992

APPLICATION NUMBER: 07/665,961

FILING DATE: 07-MAR-1991

ATTORNEY/ACENT INFORMATION:

NAME: Elbing, Karen L

REGISTRATION NUMBER: 35,238

REFERENCE/DOCKET NUMBER: 00786/2.

TELEPHONE: 617-428-0200
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
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ADDRESSEE: Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                               OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/218,950
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APPLICANT: Banapour, Be
APPLICANT: Romeo, Charl
APPLICANT: Kolanus, Wal
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                TELEFAX:
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CITY: E
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                                617-428-7045
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Romeo, Charles
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                                                                                                                                                                                                                                                                                                                                                                                                                                            Diskette
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99.5%;
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                                                                                    00786/247001
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Pred. No. 2.2e-53;
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RECEPTOR- BE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local Similarity
Matches 207; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Patent No.
PRIOR APPLICATION UNMBER: US/08/284,391
PILLING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
PILLING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILLING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILLING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGRERUCK/DOCKET NUMBER: 00786/2470
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                OPERATING SYSTEM: DOS
SOFTWARE: FRSESEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION UNMBER: US/08/394,388A
FILING DATE: 24-FEB-1995
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION UNMBER: US/08/204
                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Wir
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ADDRESSEE: Clark & E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
TITLE OF INVENTION: CELLS BY CHIMERIC CD4 RECEPTOR- BEARING
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STREET:
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5. 6753162
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Romeo, Charles
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Pred. No. 2.2e-53;
0; Mismatches 1;
                                                  00786/247001
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Patent No. 5565335
GENERAL INFORMATION:
APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
NUMBER OF SEQUENCES: 25
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          FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
PRIOR APPLICATION NUMBER: 07/104329
APPLICATION NUMBER: 07/104329
FILING DATE: 02-CCT-1997
ATTORNEY/AGENT INFORMATION:
NAME: Hasak, Janet E.
REGISTRATION NUMBER: 28,616
REGISTRATION NUMBER: 28,616
REFERENCE/DOCKET NUMBER: 444P1C
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                                                                                                                                                                                                                                   APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 07/842777
                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 1
FILING DATE: 02-MAY-:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
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TELECOMMUNICATION INFORMATION
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Pred. No. 2.2e-53;
0; Mismatches 1
                  444P1C2
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RESULT 10
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SEQUENCE CHARACTERISTICS:
LENGTH: 402 amino
Type-
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Best Local Similarity
Matches 207; Conserv
PILING DATE: 26-AUG-1992
PRIOR APPLICATION NUMBER: 07/842777
APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
PRIOR APPLICATION DATA: 19-7250785
APPLICATION NUMBER: 07/250785
FILING DATE: 28-SEP-1988
PRIOR APPLICATION NUMBER: 07/104329
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                     FILING DATE: 1-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/236
FILING DATE: 02-MAX-1994
PRIOR APPLICATION NUMBER: 07/36
                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              APPLICANT: Capon, Daniel J.
APPLICANT: Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: Genentech, Inc.
                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US/OFILING DATE: 1-JUN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: South San Francisco
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Patent No. 6710169
GENERAL INFORMATION:
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Best Local Similarity 99.5%;
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TELEX: 910/937-7168
INFORMATION FOR CO.
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                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/10/157,408
FILING DATE: 28-May-2002
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
'COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gregory, Timothy J. TITLE OF INVENTION: Adheson Variants NUMBER OF SEQUENCES: 25
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ADDRESSEE: Genente
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                                                  APPLICATION NUMBER: US/08/457,918
FILING DATE: 1-7UN-1995
APPLICATION NUMBER: 08/236311
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
APPLICATION NUMBER: 07/250785
ETITING DATE: 18-FEB-1992
APPLICATION NUMBER: 07/250785
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STREET: 460 Point San Bruno
CITY: South San Francisco
STATE: California
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FILING DATE: 28-SEP-1988
APPLICATION NUMBER: 07/104329
FILING DATE: 02-OCT-1987
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Pred. No. 2.2e-53;
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TELEPHONE: (212) 278-0400
TELEPAX: (212) 391-0525
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
                                                    CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Sweet, Richard W.
APPLICANT: Arthos, James
TITLE OF INVENTION: DERIVATIVES OF SOLUBLE
NUMBER OF SEQUENCES: 22
                                                                                                                                                                                                                                SOFTWARE: PatentIn Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Maddon, APPLICANT: Axel, R
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                                                                                                                                                                                                                                                                                                                                                                     CITY: New York
STATE: New York
COUNTRY: U.S.A.
                                                                                                                                                                                             APPLICATION NUMBER: FILING DATE:
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ZIP: 10036
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TELECOMMUNICATION INFORMATION:
TELEPHONE. 4.7.7.7.
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TYPE: amino acid
TOPOLOGY: linear
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1185 Avenue of the Americas
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Axel, Richard
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Pred. No. 2.2e
0; Mismatches
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US-08-466-368-4
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US-08-466-368-4
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Best Local Similarity
                                                                                                                                                  COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOTTWARE: Patentin Release #1.0, Version #1.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/466,368
FILING DATE: 06-JUN-1995
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: White, John P.
REFIRENCE/DOCKET NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 24577-E1-B/JPW/AKC
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
                                                                                                                     TELEFAX: 212-391-0525
INFORMATION FOR SEQ ID NO: 4:
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APPLICANT: Maddon
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APPLICANT:
                  MOLECULE TYPE: protein
                                                                            SEQUENCE CHARACTERISTICS:
LENGTH: 458 amino acid
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ADDRESSEE: Cooper &
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APPLICANT: McDougal, J. S.
TITLE OF INVENTION: DA ENCODING THE T CELL SURFACE PROTEIN
TITLE OF INVENTION: T4 AND USE OF FRAGMENTS OF T4 IN THE TREATMENT OF AIDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQUENCES:
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                                     LENGTH: 458 amino acids TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: New York
STATE: New York
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1185 Avenue of Americas
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                                                                                                                                          212-391-0525
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Axel, Richard
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Littman, Dan
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Pred. No. 2.5e-53;
0; Mismatches 1
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Query Match Best Local Similarity

39.7**%**; 99.5**%**;

Score 1059; DB 3; Pred. No. 2.5e-53;

Length 458;

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RESULT 14
US-08-417-495-5
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GENERAL INFORMATION:
APPLICANT: Seed,
                                                 Query Match
Best Local Similarity
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                                Matches 207;
                                                                                                                                                                              TELEX: 200154
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                            ATTORNEY/AGENT INFORMATION:
NAME: Clark, Paul T.
REGISTRATION NUMBER: 30,162
REFERENCE/DOCKET NUMBER: 00786/119002
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
                                                                                                                  MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: | FILING DATE: CLASSIFICATION: 435 | PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version 3.30)
SOFTWARE: Wordperfect (Version 5.0)
CURRENT APPLICATION DATA:
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MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
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TITLE OF INVENTION:
TITLE OF INVENTION:
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                                                                                                                              TYPE: amino acid
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                               APPLICATION NUMBER: 07/665,961 FILING DATE: March 7, 1991 CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
APPLICATION NUMBER: US/07/847,566
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STATE: MA
                                                                                                                                                                                                                                TELEFAX:
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                                                                                                                                                             LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
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1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
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                                                                                                                                                                                                                                  (617) 542-8906
                                  Conservative
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N: Redirection of Cellular Immunity
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                         ; Score 1059; DB 2; Le
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US-08-284-391B-5
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   Matches 207;
                   Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/284,391B
FILING DATE: 02-AUG-1994
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence
                                                                                                                                                                   INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
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APPLICANT:
APPLICANT:
                                                                                TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                                                                                                                                                                                                                                                    FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 617-428-0200
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ADDRESSEE: Clark & Elbing
STREET: 176 Federal Street
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                                                                                                                                                                                                                                                                     NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,
REFERENCE/DOCKET NUMBER:
                                                                                                                 STRANDEDNESS:
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Romeo, Charles
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   Conservative
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                   39.7%;
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Pred. No. 2.5e-53;
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Search completed: November 21, 2004, 13:44:45 Job time : 66.8175 secs	181 TWTCTVLQNQKKVEFKIDIVVLAFQKAS 208	181 TWTCTVLQNQKKVEFKIDIVVLAFQKAS 208	121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180	121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180	61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120	61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFFLIIKNLKIEDSDTYICEVEDQKEEVQL 120	MRRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Title:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq length: 0
seq length: 2000000000
Published Applications AA:*

1: /cgn2=6/ptodata/2/pubpaa/US07 PUBCOMB.pep:*

2: /cgn2=6/ptodata/2/pubpaa/US06 NEW PUB.pep:*

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5: /cgn2=6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*

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6: /cgn2=6/ptodata/2/pubpaa/US08_NEW PUB.pep:*

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gapop 10.0 , Gapext 0.5
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Copyright (c) 1993 - 2004 Compugen Ltd.
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

13	12	11	10	9	89	7	6	ъ	4.	ω	2	۳	Result No.
1059	1059	1059	1059	1059	1059	1062	1062	1062	1064	1064	1064	1064	Score
39.7	39.7	39.7	39.7	39.7	39.7	39.8	39.8	39.8	39.9	39.9	39.9	39.9	Query Match 1
462	457	402	402	402	398	458	458	458	458	458	458	458	Query Match Length DB
10	11	17	14	14	10	14	10	8	14	14	14	14	: B
US-09-939-537-5	US-09-891-119A-9	US-10-769-247-1	US-10-097-044A-1	US-10-157-408-1	US-09-939-537-29	US-10-092-138-25	US-09-230-111C-25	US-08-681-219-27	US-10-207-655-170	US-10-188-444-39	US-10-103-597A-39	US-10-151-274-3	ID
5,	Sequence 9, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 1, Appli	Sequence 29, Appl	Sequence 25, Appl	Sequence 25, Appl	Sequence 27, Appl	Sequence 170, App	Sequence 39, Appl	Sequence 39, Appl	Sequence 3, Appli	Description

	44	43	42	41	40	39	38	37	36	35	34	33	32	31					26	25	24	23	22	21	20	19	18	17	16	15	1
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34.4	•	34.4	34.6	34.6	34.6	34.7	34.8	35.2	35.4	35.5	35.5	35.5	35.8	35.8	35.9	35.9	36.0	36.0	38.8	39.3	39.3	39.4	39.4	39.4	39.4	39.5	39.7	39.7	39.7	39.7	07.1
476	453	450	720	720	590	788	621	370	448	434	434	434	251	251	246	246	250	250	203	310	310	432	432	530	530	397	575	575	532	532	707
17	17	17	9	9	9	14					14	14	14	10	14	10	14	10	10	9	œ	ø	œ	9	œ	1	1	10	11	10	F
US-10-768-932A-6	US-10-768-932A-8		US-09-934-060A-4	09-934-060A-	US-09-934-060A-13	US-10-073-118-26		US-09-759-841-6	US-10-024-329-32	US-10-769-247-4	0-097	-10-157-4	-10-293-418-12	-880-748-12	US-10-293-418-1268	09-880-748-12	10-293-418-19	09-880-748-19	09-939-	09-766-9	8-485-3	US-09-766-995-2		US-09-766-995-4	US-08-485-163-5	US-09-891-119A-2	US-09-243-008-4	09-939-537-	09-243-008-	09-939-537	00 07 640 000 0
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ALIGNMENTS

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; TYPE: PRT
; ORGANISM: Homo sapiens
US-10-151-274-3
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                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION NUMBER: US/09/517,605
PRIOR FILING DATE: 2000-03-02
NUMBER OF SEQ ID NOS: 17
SOFTWARE: Patentin Ver. 2.0
SEQ ID NO 3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Sequence 3, Application US/10151274
Publication No. US20030064071A1
GENERAL INFORMATION:
APPLICANT: Littman, Dan R.
APPLICANT: Kwon, Douglas S.
APPLICANT: Work, Douglas S.
                                                                                                                                                                                    Matches 208;
                                                                                                                                                                                                                              Query Match
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APPLICANT: Geijtenbeck, Tneo
TITLE OF INVENTION: INTO
TITLE OF INVENTION: INTO
TITLE OF INVENTION: CELLS
FILE REFERENCE: 1049-1-017
CURRENT APPLICATION NUMBER: US/10/151,274
CURRENT FILING DATE: 2002-05-20
                                                                                                                                                                               Match 39.9%; Score 1064; DB 14; Local Similarity 100.0%; Pred. No. 7.9e-51; es 208; Conservative 0; Mismatches 0;
                            61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKVLKIEDSDTYICEVEDQKEEVQL 120
  61
                                                                                                                 1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                                                                       MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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US-10-103-597A-39
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CURRENT APPLICATION NUMBER: US/10/103,597A
CURRENT FILING DATE: 2002-10-17
PRIOR APPLICATION NUMBER: PCT/GB00/03579
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: GB 9922352.1
PRIOR APPLICATION NUMBER: GB 9922352.1
PRIOR FILING DATE: 1999-09-21
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FastSEQ for Windows Version 4.0
                                                                                                                                                                                                                                                                                                           US-10-188-444-39
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                                                                                                                                                                 Sequence 39, Application US/10188444
publication W. US2003010435A1
GENERAL INFORMATION:
APPLICANT: Jakobsen, Bent Karsten
TITLE OF INVENTION: Screening Methods
FILE REFERENCE: 102286.142 (CIP)
CURRENT APPLICATION NUMBER: US/10/188,444
CURRENT FILING DATE: 2002-07-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 39, Application US/10103597A
Publication No. US20030096432A1
GENERAL INFORMATION:
APPLICANT: Jakobsen, Bent Karsten
TITLE OF INVENTION: Screening Methods
                                              PRIOR APPLICATION NUMBER: PCT/GB00/03579
PRIOR FILING DATE: 2000-09-18
PRIOR APPLICATION NUMBER: GB 9922352:1
PRIOR FILING DATE: 1999-09-21
NUMBER OF SEQ ID NOS: 39
SOFTWARE: FBETSEQ for Windows Version 4.0
SEQ ID NO 39
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ORGANISM: Homo sapiens
                LENGTH: 45
TYPE: PRT
ORGANISM: Homo sapiens
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Local Similarity 100.0%;
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; Pred. No. 7.9e-51;
n: Mismatches 0;
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   NUMBER OF SEQUENCES:
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APPLICANT: Hayden-Ledbetter, Martha S.
APPLICANT: Hayden-Ledbetter, Martha S.
TITLE OF INVENTION: BINDING DOMAIN-IMMUNOGLOBULIN FUS:
FILE REFERENCE: 390069.401C1
CURRENT APPLICATION NUMBER: US/10/207,655
CURRENT FILING DATE: 2002-07-25
NUMBER OF SEQ ID NOS: 426
SOFTWARE: Patentin version 3.0
SEQ ID NO 170
LENGTH: 458
TYPE: PRT
ORGANISM: Homo sapiens
US-10-207-655-170
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US-10-207-655-170
                                                                                                                                   US-08-681-219-27
Sequence 27, Application US/08681219
Publication No. US20020058607A1
GENERAL INFORMATION:
APPLICANT: Takaaki Sato and Junn
TITLE OF INVENTION: COMPOUNDS THI
TITLE OF INVENTION: (PDZ/DHR) DOI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 170, Application US/10207655 Publication No. US20030118592A1 GENERAL INFORMATION:
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Best Local Similarity
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Takaaki Sato and Junn Yanagiaawa
VENTION: COMPOUNDS THAT INHIBIT THE INTERACTION
VENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLG
VENTION: (PDZ/DHR) DOMAIN AND USES THEREOF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             39.9%; Score 1064; DB 14; 100.0%; Pred. No. 7.9e-51;
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CORRESPONDENCE ADDRESS:

ADDRESSEE:

E: Cooper & Dunham LLP 1185 Avenue of the Americas

CITY: New York STATE: New York

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RESULT 6
US-09-230-111C-25
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; TYPE: PRT ; ORGANISM: human US-09-230-111C-25
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                                            APPLICANT: Sato, Taka-Aki
APPLICANT: Yanagisawa, Junn
APPLICANT: Yanagisawa, Junn
TITLE OF INVENTION: COMPOUNDS THAT INHIBIT INTERACTION BETWEEN
TITLE OF INVENTION: SIGNAL-TRANSDUCING PROTEINS AND THE GLGF (PDZ/DHR)
TITLE OF INVENTION: DOWALN AND USES THEREOF
FILE REFERENCE: 48962-A-PCT-US
CURRENT APPLICATION NUMBER: US/09/230,111C
CURRENT APPLICATION NUMBER: US/09/230,111C
CURRENT FILING DATE: 1999-05-17
NUMBER OF SEQ ID NOS: 33
SOFTWARE: PATENTIN VEY: 2.1
SEQ ID NO 25
LENGTH: 458
TWORL DOT
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NAME: White, John P
REGISTRATION NUMBER: 28,678
REFERENCE/DOCKET NUMBER: 0575,
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 278-0400
TELEPHONE: (212) 391-0525
INFORMATION FOR SEQ ID NO: 27:
SEQUENCE CHARACTERISTICS:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                     Sequence 25, Application US/09230111C Publication No. US20030203414A1 GENERAL INFORMATION:
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Best Local Similarity
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OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/681,219
FILING DATE: 22-JUL-1996
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
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99.5%;
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Pred. No. 1e-50;
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RESULT 8
US-09-939-537-29
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US-10-092-138-25
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LENGTH: 458
TYPE: PRT
ORGANISM: human
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Publication No. US20030170723A1
GENERAL INFORMATION:
APPLICANT: Sato, Taka-Aki
TITLE OF INVENTION: METHOD OF PREPARING A PROTEIN ARRAY BASED ON
TITLE OF INVENTION: BICCHEMICAL PROTEIN-PROTEIN INTERACTION
FILE REFERENCE: 65823/JDW/PT
CURRENT APPLICATION NUMBER: US/10/092,138
CURRENT FILING DATE: 2002-09-06
NUMBER OF SEQ ID NOS: 33
SOFTWARE: Patentin Ver. 2.1
                                                                                         Sequence 29, Application US/09939537
Publication No. US20030138410A1
GENERAL INFORMATION:
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Best Local Similarity 99.5
Matches 207; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
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                 TITLE OF
                                                                              APPLICANT: Seed, Brian
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Banapour, Babak
Romeo, Charles
Kolanus, Waldemar
KOLANTION: TARGETED C
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Pred. No. 1e-50;
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Pred. No. 1e-50;
1; Mismatches 0;
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   CYTOLYSIS OF HIV-INFECTED CHIMERIC CD4 RECEPTOR- BEA
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   BEARING
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STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
SEQUENCE DESCRIPTION: SEQ ID NO:
US-09-939-537-29
                                                                                               RESULT 9
US-10-157-408-1
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                                              Sequence 1, Application US/10157408 Publication No. US20030104535A1 GENERAL INFORMATION:
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Best Local :
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INFORMATION FOR SEQ ID NO: 29:
SEQUENCE CHARACTERISTICS:
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les 207; Conserv
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CORRESPONDENCE ADDRESS:
Clark & Elbing LLP
STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,537
FILING DATE: 24-Aug-2001
CLASSIFICATION: <Unknown>
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MEDIUM TYPE: Diskette
COMPUTER: 1EM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/284,391
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
APPLICANT: Capon, Daniel J.
Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/247001
TELECOMMUNICATION INFORMATION:
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STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                  ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                                                                                                                                   TWTCTVLQNQKKVEFKIDIVVLAFQKAS
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APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: amino acid
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TELEFAX: 617-428-7045
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Pred. No. 1.3e-50;
0; Mismatches 1
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RESULT 10
US-10-097-044A-1
US-10-097-044A-1
; Sequence 1, Application US/10097044A
; Publication No. US20030143220A1
; Publication No. US20030143220A1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-10-157-408-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches 207;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match 39.7%;
Best Local Similarity 99.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO: 1:
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CORRESPONDENCE ADDRESS:
ADDRESSE: Genentech, Inc.
STREET: 460 Point San Brunc
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE: patin (Genentecn)
CURRENT APPLICATION NUMBER: US/10/157,408
APPLICATION NUMBER: US/10/157,408
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
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MEDIUM TYPE: 5.25 inch,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
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IOR APPLICATION DATA:

PILING DATE: 1-JUN-1995

APPLICATION NUMBER: US/08/457,918

FILING DATE: 1-JUN-1995

APPLICATION NUMBER: 08/236311

FILING DATE: 02-MAY-1994

APPLICATION NUMBER: 07/936190

FILING DATE: 26-AUG-1992

APPLICATION NUMBER: 07/842777

FILING DATE: 18-FEB-1992

APPLICATION NUMBER: 07/250785

FILING DATE: 18-FEB-1996

APPLICATION NUMBER: 07/250785

FILING DATE: 28-SEP-1988

APPLICATION NUMBER: 07/104329

FILING DATE: 02-OCT-1987
                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                                                                                                                                                                                        TWTCTVLQNQKKVEFKIDIVVLAFQKAS 208
                                                                                                                                                                                                                                                                                                                                                                                          ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                      MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                        TWTCTVLQNQKKVEFKIDIVVLAFQKAS
                                                                                                                                                                                                                                                             LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                   ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: amino acid TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 402 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0444P1C3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME: Kubinec, Jeffro
REGISTRATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE: 28-May-2002
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Pred. No. 1.3e-50;
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APPLICANT: Capon, Daniel J.

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RESULT 11
US-10-769-247-1
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Sequence 1, Application US/10769247 Publication No. US20040197809A1
                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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Best Local Similarity 99.5%;
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0444P1C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SEQUENCE DESCRIPTION: SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: patin (Genentech)
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gregory, Timothy J.
TITLE OF INVENTION: Adheson Variants
NUMBER OF SEQUENCES: 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PRIOR
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ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
                                                                                                                                                           181
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                                                                                                                                                                                                  121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                                                                                                                                                                                                                                                                                                                                              1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/08/457,918
FILING DATE: 1-JUN-1995
APPLICATION NUMBER: 08/236311
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
                                                                                                                                               TWTCTVLQNQKKVEFKIDIVVLAFQKAS
                                                                                                                                                                                                                                                                                                           ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTVICEVEDQKEEVQL 120
                                                                                                                  TWTCTVLQNQKKVEFKIDIVVLAFQKAS
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                                                                                                                                                                                                                                                                            ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICATION NUMBER: 07/250785 FILING DATE: 28-SEP-1988
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICATION NUMBER: US/10/097,044A FILING DATE: 28-May-2002
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: 415/952-9881
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                                                                                                                                                                                                                                                                                                                                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 1059; DB 14; Length 402; Pred. No. 1.3e-50;
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RESULT 12
US-09-891-119A-9
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; SEQUENCE DESCRIPTION: SEQ ID NO: 1: US-10-769-247-1
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Best Local Similarity 99.5%;
Matches 207; Conservative
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INFORMATION FOR SEQ ID NO: 1:
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APPLICANT: Capon, Daniel J.
GEGGOTY, Timothy J.
TITLE OF INVENTION: Adheson Variants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE: 28-SEP-1988
APPLICATION NUMBER: 07/104329
FILING DATE: 02-OCT-1987
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME: Kubinec, Jeffrey S.
REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: P0444P1C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PILING DATE: 30-Jan-2004
CLASSIFICATION: <Unknown>
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE: patin (Gen CURRENT APPLICATION DATA:
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CORRESPONDENCE ADDRESS:
181
                                      181 TWTCTVLQNQKKVEFKIDIVVLAFQKAS 208
                                                                                            121
                                                                                                                         121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
                                                                                                                                                                                                                                    61
                                                                                                                                                                                    61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                                                                                                                                                                                                                                                                             1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                                                                                                                                                                                                                                                                1 MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICATION NUMBER: US/08/457,918
FILING DATE: 1-JUN-1995
APPLICATION NUMBER: 08/236311
FILING DATE: 02-MAY-1994
APPLICATION NUMBER: 07/936190
FILING DATE: 26-AUG-1992
APPLICATION NUMBER: 07/842777
FILING DATE: 18-FEB-1992
APPLICATION NUMBER: 07/250785
APPLICATION NUMBER: 07/250785
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                                                                                            LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
                                                                                                                                                                                                                   ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
TWTCTVLQNQKKVEFKIDIVVLAFQKAS 208
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FILING DATE: 30-Jan-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: 5.25 inch, 360 Kb floppy disk
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                                                                                                                                                                                                                                                                                                                                                                          0;
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Pred. No. 1.3e-50;
0; Mismatches 1
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; LENGTH: 457
; TYPE: PRT
; ORGANISM: human
US-09-891-119A-9
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US-09-939-537-5
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APPLICANT: Maddon, Paul J.
APPLICANT: Maddon, Paul J.
TITLE OF INVENTION: DERIVATIVES OF SOLUBLE T-4
FILE REFERENCE: 24577-CY-B
CURRENT APPLICATION NUMBER: US/09/891,119A
CURRENT FILING DATE: 201-06-25
NUMBER OF SEQ ID NOS: 22
SOFTWARE: PatentIn version 3.1
SEQ ID NO 9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5, Application US/09939537
Publication No. US20030138410A1
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Sequence 9, Application US/09891119A Publication No. US20040013683A1
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Matches
                                                                                                                                    COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,537
FILING DATE: 24-Aug-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                       ZIP: 02110
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Clark & Elbing LLP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Kolanus, waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Seed, Brian
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 TWTCTVLQNQKKVEFKIDIVVLAFQKAS 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            207;
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                                                                                                                                                                                                                                                                                                                                                                    STATE: MA
COUNTRY: USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
APPLICATION NUMBER: 07/665,961
                                                        APPLICATION NUMBER: 08/284,391
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
                                                                                                                                                                                                                                                                                                                                                                                                          STREET: 176 Federal Street
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Banapour, Babak
Romeo, Charles
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MOLECULE TYPE: protein seQuence Description: SeQ ID NO: US-09-939-537-5
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US-09-243-008-5
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Publication No. US20040005334A1
GENERAL INFORMATION:
APPLICANT: Seed, Brian et al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Matches
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Best Local Similarity
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TELEX: <UNKNOWN>
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                           APPLICATION NUMBER: US/09/243,008 FILING DATE: 02-Feb-1999 PRIOR APPLICATION DATA: APPLICATION NUMBER: US/08/394,176 FILING DATE: SEPTEMBER 11,1995 APPLICATION NUMBER: 08/203,866 FILING DATE: February 28, 1994 APPLICATION NUMBER: 07/847,566
                                                                                                                                                                                                         COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5" Diskette, 1.44 Mb
COMPUTER: IBM PS/2 Model 50Z or 55SX
OPERATING SYSTEM: IBM P.C. DOS (Version
SOFTWARE: Wordperfect (Version 5.0)
                                                                                                                                                                                                  CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: 617-428-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ATTORNEY/AGENT INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE OF INVENTION: Redirection of Cellular Immunity by Receptor Chimeras
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             181
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REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/247001
             APPLICATION NUMBER: FILING DATE: March (APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                             STATE: MA
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TYPE: amino acids
                                                                                                                                                                                                                                                                                                                                                                   CITY: Boston
                                                                                                                                                                                                                                                                                                                                                                                  STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE: Fish & Richardson P.C.
FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                                    225 Franklin Street
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                 March 6, 1992
WUMBER: 07/665,961
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Pred. No. 1.5e-50;
0; Mismatches 1
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ATTORNEY/AGENT INFORMATION:

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RESULT 15
US-09-939-537-6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match
Best Local Similarity
Matches 207; Conserv
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Seed, Brian
Banapour, Babak
Banapour, Babak
Romeo, Charles
Kolanus, Waldemar
TITLE OF INVENTION: TARGETED CYTOLYSIS OF HIV-INFECTED
CELLS BY CHIMERIC CD4 RECEPTOR- BEARING CELLS
                                                                                                                      COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FASTSEQ for Windows Version
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/939,537
FILING DATE: 24-Aug-2001
CLASSIFICATION: «Unknown»
PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: protein SEQUENCE DESCRIPTION: SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                          CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Karen F. Lech, Ph.D
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786/270001
TELECOMMUNICATION INFORMATION:
TELEPHONE: (617) 542-5070
TELEFAX: (617) 542-8906
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APPLICATION NUMBER: 08/284,391
FILING DATE: 02-AUG-1994
APPLICATION NUMBER: 08/195,395
FILING DATE: 14-FEB-1994
APPLICATION NUMBER: 07/847,566
FILING DATE: 06-MAR-1992
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                                                                                                                                                                                                                                                                                                                                                                            CITY: Boston
STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Clark & Elbing LLP STREET: 176 Federal Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               LENGTH: 462 amino acids
TYPE: amino acid
                                                                                                                                                                                                                                                                                                                                                         COUNTRY: USA
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; SEQUENCE DESCRIPTION: SEQ ID NO: 6:
US-09-939-537-6
                                                                                                                                                                                                                                                                                                                                                                                           Query Match 39.7%;
Best Local Similarity 99.5%;
                                                                                                                                                                                                                                                                                                                                                                        Matches 207;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICATION NUMBER: 07/665,961
FILING DATE: 07-MAR-1991
ATTORNEY/AGENT INFORMATION:
NAME: Elbing, Karen L
REGISTRATION NUMBER: 35,238
REFERENCE/DOCKET NUMBER: 00786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELECOMMUNICATION INFORMATION:
                                                          181
                                                                                                 181
                                                                                                                                       121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                          121 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG 180
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                                                                                     TWTCTVLQNQKKVEFKIDIVVLAFQKAS 208
                                                                                                                                                                                                                                                       ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                          TWTCTVLQNQKKVEFKIDIVVLAFQKAS
                                                                                                                                                                                                                ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                             MNRGVPFRHLLLVLQLALLPAATQGNKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          LENGTH: 532 amino acids
TYPE: amino acid
STRANGENESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEFAX: 617-428-7045
TELEX: <Unknown>
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2004, 14:03:56
                                                                                                                                                                                                                                                                                                                                                                        0,
                                                                                                                                                                                                                                                                                                                                                                      Score 1059; DB 10;
Pred. No. 1.7e-50;
0; Mismatches 1;
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                                                                                                                                                                                                                                                                                                                                                                                                           Length 532;
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Search completed: November 21, Job time: 227.482 secs

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Minimum DB
Maximum DB
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Listing first 45 summaries
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Copyright (c) 1993 - 2004 Compugen Ltd.
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                                  AAR95062

AAW19543

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AAW202127

AAY33597

AAY33597

AAY43496

AAW43210

AAW62210

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AAR34034
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Aar34034 Linking s
Aar95062 ScFv sppac
Aaw17094 Gly(4)-Se
Aaw17094 Gly(4)-Se
Aaw19543 Chimeric
Aay02537 IFNAR2/IF
Aay33597 VH-VL dom
Aay43496 Linker fo
Aay83210 Peptide 1
Aab06226 Expressio
Aay83710 Linker us
Aab14535 Peptide 1
Aab014535 Peptide 1
Aab0156 Linker us
Aab14535 Peptide 1
                            Aae11873
Aab57374
Abb56480
Aag62343
Aab50848
Aab57784
Aab55527
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Linker pe
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Flexible
Peptide 1
Linker pe
Linker pe
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SQ	រុក្សស្តុក្សស្តុ	X PS	X P P	X R X	X P S	X P	X R R	X P S	X B i	X P i	ž S ž	X	X H	X Z I	X & I	RES AAR ID																
Sequence 5 AA;	A dispersible apo A-I/B-100 fusion polypeptide is claimed which a first AA sequence of apo A-I (see AAR72605) and that includes AA sequence positions 120-135 (see AAR72606). The two sequences operatively linked. An exemplary linking sequence is AAR72707 whencoding DNA can be ligated between an apo A-I and a B-100 encodes sequence.	PS Disclosure; Col 18; 41pp; English. XX	Polypeptide mimic of native apo B-100 and native apo A-I - usef assays for LDL and HDL in plasma samples.	DR WPI; 1993-134378/16.	YY Witztum JL, Koduri KR, Young SG, Smith RS, Curtiss LK;	PA (SCRI) SCRIPPS RES INST. XX	PR 09-OCT-1991; 91US-00774633. PR 18-JUN-1992; 92US-00901706. YX	PF 08-OCT-1992; 92US-00959946. XX	PD 18-APR-1995. XX	PN US5408038-A. XX	OS Synthetic.	KW Apo A-I; LDL cholesterol; low density lipoprotein; fusion polypept KW linker.	DE Linker for apo A-I and apo B-100 fusion polypeptide. XX	DT 31-OCT-1995 (first entry)	AC AAR72707;	RBSULT 1 AAR72707 ID AAR72707 standard; peptide; 5 AA. XX	ALIGNMENTS	28 100.0 5 5 AAU75495 Aau75495	28 100.0 5 5 AAE25959 Aae25959	28 100.0 5 5 AAE19822 Aae19822	28 100.0 5 5 AAO14387 Aao14387	28 100.0 5 5 ABP48193 Abp48193	28 100.0 5 5 ABJ05006 Abj05006	0 5 5 ABP52872 Abp52872	28 100.0 5 5 ABB79970 Abb79970	28 100.0 5 5 AAU76043 Aau76043	28 100.0 5 5 ABG31871 . Abg31871	28 100.0 5 4 AAE08730 Aae08730	28 100.0 5 4 AAB68571 Aab68571	28 100.0 5 4 AAG63011 Aag63011	28 100.0 5 4 AAU051/3 Aau051/2 Aau051/2	30 100 0 5 A NATIONEL 23
	ch contains es at least es are whose coding DNA		eful in									ypeptide;						Human Gl	9 Linker pe	2 Linker pe	7 Linker pe	3 Peptide 1	6 VH and VL	Flexibl	0 Linker pe	Synthet	Spacer p	Peptide	11 Linker pe	Peptide	Pain	03:3

Query Match 100.0%; Score 28; DB 2; Best Local Similarity 100.0%; Pred. No. 1.7e+06; Matches 5; Conservative 0; Mismatches 0;

Length 5; ;;); Indels

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Gaps

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RESULT 2
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ID AAR3
XX AAR3
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AC Link
DT 13-A
XX Link
DE Link
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XX Lipo
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XX W09-C
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RESULT 3
AAR95062
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18-JUN-1992;
08-OCT-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          The inventors claim a portion of the polypeptide contg. apo B-100 that immunoreacts with antibodies secreted by the hybridoma MB47 having ATCC Accession No. 8746. Polypeptides specifically claimed include residues 217-297, 216-310, 216-331, 216-352, 216-377, 1-377, 205-297, 173-297, 140-297. DNA sequences encoding the polypeptides are also claimed. Also claimed are a fusion polypolypeptide that contains: (a) a first amino acid residue sequence up to 250 residues in length that includes residues 120-135 of apo A-I, (b) a second amino acid residue sequence up to 375 residues in length that includes residues 217-297 of apo B-100 and DNA encoding it. (Updated on 25 MAR-2003 to correct PN field.) (Updated on 25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Polypeptide mimic of native apo B-100 and native assays for LDL and HDL in plasma samples.
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13-AUG-1993
                               18-AUG-1996
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                                                                                     AAR95062;
                                                                                                                                      AAR95062 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              15-APR-1993.
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                               (first entry)
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92US-00901706.
92US-00959946.
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Pred. No. 1.7e+06;
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RRESULT 4
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DT 14-S
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Haem
KW Haem
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Synt
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PF 04-C
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Matches 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A flexible spacer peptide (AAR95062) is used to link the light chain variable domain to the heavy chain variable domain of a single chain recombinant antibody (scFv). The scFv may be derived from a monoclonal antibody, e.g. MAb FRP5, and forms the ligand domain of a multidomain protein (see also AAR95053 and AAR95056-58) that is used with an effector nucleic acid in a novel nucleic acid transfer system suitable for gene therapy. The ligand domain has a target cell recognition function and allows cellular internalization of the multidomain protein/nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nucleic acid transfer system; gene transfer; cell targeting; multidomain protein; vector; single chain antibody.
                                                                                                                                     Haematopoietic protein; human; granulocyte-colony stimulating factor; G-CSF; interleukin; c-mpl ligand; likker; gene therapy; aplastic anaemia; stem cell expansion; leukopaenia; neutropaenia; vector; bone marrow; thrombocytopaenia; blood cell activation; growth.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acid transfer system includes toxin translocation cell.
                                                                                                                                                                                                             Gly(4)-Ser linker peptide for chimeric protein construct.
                                                                                                                                                                                                                                                                                              AAW17094 standard; peptide; 5 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             09-MAY-1996
                             04-OCT-1996;
                                                                                                              Synthetic
                                                                                                                                                                                                                                        14-SEP-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Page 8; 106pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1996-239505/24.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Wels W,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      01-NOV-1994;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    scfv spacer peptide.
                                                        10-APR-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (VELS/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WELS
                                                                                                                                                                                                                                                                                                                                                                                                                       h 100.0%;
Similarity 100.0%;
5; Conservative 0
                                                                                                                                                                                                                                                                                                                                                                                             egges 5
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                                                                                                                                                                                                                                        (first entry)
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                             96WO-US015774.
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                                                                                                                                                                                                                                                                                                                                                                                                                          <u>,</u>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          for gene therapy, e.g. against cancer - domain to target nucleic acid to specific
                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 28;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                      1.7e+06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                    DB 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            gene therapy;
cancer; scFv;
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length 5;
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05-OCT-1995;

95US-0004834P

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PA (YIS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  The invention relates to a novel haematopoietic protein (HP) comprising CC an amino acid (AA) sequence of formula; R1-L1-R2; R2-L1-R1; R1-R2; or R2-CC R1; where R1 and R2 are independently selected from: (I) a modified human CC granulocyte-colony stimulating factor (HG-CSF) AA sequence; (II) a cc modified human interleukin-3 (hIL-3) AA sequence; (II) a modified human CC cmpl ligand; and a colony stimulating factor (CSF); and L1 = a linker CC capable of linking R1 to R2. This sequence represents an example of a CC linker used to construct the proteins of the invention. Vectors CC comprising the nucleic acid molecules are useful for the recombinant CC production of HP. The nucleic acid molecules are useful in gene therapy. CC The HP's are useful for stimulating the production of haematopoietic CC cells in patients, selective ex vivo expansion of stem cells and for C reatment of haematopoietic directive include leukopaenia, neutropaenia, aplastic anaemia and construct of the colon cell activation and growth before infusion into the construct.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
Best Local :
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Matches
             WPI; 1997-298116/27
                                       Lorberboum-Galski H,
Yarkoni S;
                                                                                                           17-NOV-1995;
26-DEC-1995;
                                                                                                                                                                                 29-MAY-1997
                                                                                                                                                                                                          W09719179-A1
                                                                                                                                                                                                                                        Synthetic
                                                                                                                                                                                                                                                                 Pseudomonas exotoxin; myelin basic protein; chimeric protein; autoimmune disease; multiple sclerosis; human.
                                                                                                                                                                                                                                                                                                        Chimeric protein pentapeptide linker for the MBP moiety and PE moiety.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Sequence 5 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Multi-functional haematopoietic receptor agonists production of haematopoietic cells in patients.
                                                                                                                                                     17-NOV-1996;
                                                                                                                                                                                                                                                                                                                                       19-FEB-1998
                                                                                                                                                                                                                                                                                                                                                                                            AAW19543 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure;
                                                                                (YISS ) YISSUM
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Similarity 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Staten NR,
L, Mckearn
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                RES & DEV CO
                                                                                                           95IL-00116044.
95IL-00116559.
                                                                                                                                                     96WO-IL000151
                                                                                                                                                                                                                                                                                                                                                                                            peptide;
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                                                    Steinberger
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   m CM,
Klein
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Pred. No.
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BK, Lee SC,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Mismatches
                                                    H
                                                    Beraud
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Mcwherter
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                                                    Marianovsky I;
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RESULT 6
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        interferon-inducible protein; platelet factor 4; anti-angiogenic;
anti-tumor; multifunctional protein; angiogenic-mediated disease; cancer;
diabetic retinopathy; macular degeneration; arthritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       portion; (d) amino acids 143-168 of human MBP or an antigenic portion; and (e) an amino acid sequence in which one or more amino acids have bee deleted, added, substituted or mutated in the amino acid sequences of (a), (b), (c), or (d), the modified sequences retaining at least 75% homology with the amino acid sequences. The present sequence represents the preferred pentapeptide linker used to link the MBP moiety and PE moiety in a chimeric proteins can be used for the treatment of autoimmune diseases such as multiple sclerosis. The chimeri proteins can specifically target and kill MBP specific T cells while
                                                                                                                                                                                                      New multifunctional proteins useful for treating angiogenic-mediated
                                                                                                                                                                                                                                                                                                                                                        Bolanowski
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 01-OCT-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         30-SEP-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAY02127 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 5 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Angiostatin; endostatin; interferon; thrombospondin;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Peptide linker used to make multifunctional proteins.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY02127;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 6; Page 29;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Pseudomonas exotoxin-myelin basic protein chimeric proteins - for the treatment of auto:immune diseases, particularly multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 having no effect on non-target cells
                                                                                                                                                                                                                                                                                                                                                                                                                      SEAR ) SEARLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               cell production;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      <u>ح</u>
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                                                                                                                                                                                                                                                                                                                                                           Caparon MH,
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100.0%; Pred. No. 1.7
cive 0; Mismatches
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                                                                                                                                                                                                                                                                                                                                                           Casperson GF,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1.7e+06;
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                                                                                                                                                                                                                                                                                                                                                           Gregory SA,
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                                                                                                                                                                                                                                                                                                                                                           Klein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0;
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The specification describes multifunctional proteins which comprise combinations of angiostatin, endostatin, interferon, thrombospondin interferon-inducible protein and platelet factor 4, and have anti-

thrombospondin,

Disclosure; Page 111; 121pp;

English

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RESULT 7
AAY25357
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Best Local :
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                                 This invention describes a novel method for prolonging the in vivo effect of type I interferon (IFN) by administering IFN as a complex (A) with a subunit (I) of the human interferon alpha/beta receptor (IFNAR). The product of the invention has antiviral, anticancer, immunomodulatory, anti-arthritic and antidiabetic activity. (A) have the antiviral, anticancer and immunomodulating activities of IFN, e.g. for treating hepatitis and other viral infections, hairy cell leukemia, Kaposi's sarcoma, multiple myeloma and other cancers, multiple sclerosis, rheumatoid arthritis, mysathenia gravis, diabetes, acquired immune deficiency syndrome and lupus. When complexed in (A), the storage life of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IFNAR2; IFN-beta; type I interferon; IFNAR/IFN complex; IFN; antiviral; human interferon alpha/beta receptor; anticancer; immunomodulatory; anti-arthritic; antidiabetic; treatment; hepatitis; viral infection; hairy cell leukemia; Kaposa's sarcoma; multiple myeloma; cancer; lupus; diabetes; multiple sclerosis; rheumatoid arthritis; myasthenia gravis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tepper M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                19-DEC-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                18-DEC-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ) ARS APPI
MCINNIS
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          is stabilized against oligomerization,
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                                                This sequence represents a novel single-chain molecule (I) that binds CC multiple antigens and comprises two variable domains of heavy CC immunoglobulin chains (VH), having specificities A and B and two variable domains of light chains (VH), also with specificities A and B. The CC domains are provided as two VH-VL constructs which are attached via a peptide (P). Any VH and VL may be replaced by their functional fragments. CC The products of the invention have anticancer, antiviral, antibacterial, antimalarial and antiinflammatory activity. (I) are used to treat, CC prevent or diagnose tumors (e.g. as tumor vaccines), autoimmune diseases and inflammation (e.g. transplant rejection and arthritis) blood CC disorders (e.g. of the coagulation and/or circulatory systems, such as anemia, leucopenia, thrombocytopenia and hypertension), nervous system CC antimalarion (e.g. include a fusogenic and hypertension) reproduced simply and in predominantly homogeneous form, in a wide cvariety of hosts, either in secreted or membrane-bound forms. This cc sequence represents a VH-VL domain linker peptide which is used to construct the method of the invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         20-DEC-1999
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Pred. No.
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                                                                                                                                                                                                                                                                                        The present sequence represents a linker used to join the avb3 antagonist cand the metastasis-associated receptor ligand, in the pharmaceutical compounds of the invention. These compounds are dual avb3 receptor/metastasis-associated receptor ligands, and inhibit angiogenesis and thus proliferation of (cancer) cells. One component binds to the avb3 receptor and the other to a metastasis-associated receptor. The avb3 antagonists may also be conjugated to anti-angiogenic proteins, such as IFW-alpha and its derivatives. The compounds are used to treat angiogenesis-related disorders (mediated by the avb3-integrin), specifically cancer (of lung, breast, ovary, prostate, stomach, colon, kidney or bladder, also melanoma, hepatcoma, sarcoma and lymphoma), cartificial and macular degeneration, and also diabetic retinopathy, hemangioma, psoriasis, osteoporosis, thrombosis, angina, atherosclerosis etc. The compounds may also be useful as antiviral, antibacterial and
                                                                                                       Query Match
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Matches 5
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associated receptor, for treating angiogenesis-related diseases,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-620196/53.
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                                                                                                                                    Local Similarity
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                                                                                                                                                                                                                                                                            agents
                                                                                                          Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           peptide; 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treating angiogenesis-related
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Pred. No. 1.7e+06;
, Mismatches 0;
                                                                                                                                 Score 28; DB 2;
Pred. No. 1.7e+06;
                                                                                                       Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antagonist;
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                                                                                                                                                           Length 5;
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RESULT 10
AY83210
ID AAY83
XX AA983
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XX Bicon
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KW Bicon
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                                                                                                                                                                          leukaemia, malignant melanoma and Karposi's Barcoma. Multi-functional bioconjugates comprising both a vb 3 antagonists and interferon alpha 2b can exhibit greater biological activity when compared to a single factor or having improved half-life or decreased adverse side effects, or a combination of these properties. They can be used for inhibiting elevated levels of tumor antigens, inhibiting the proliferation of tumor cells and inhibiting tumor growth. The bioconjugates can also be used for treating e.g. osteoporosis, humoral hypercalcemia of malignancy, Paget's disease, retinopathy including diabetic retinopathy, arthritis, including rheumatoid arthritis, periodontal disease, psoriasis, thrombosis, angina, atherosclerosis, smooth muscle cell migration and restenosis in a mammal.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          cancer, arthritis, or macular degeneration. The a vb 3 integrin is normally associated with endothelial cells but can promote the formation of blood vessels (angiogenesis) in tumours. The a vb 3 integrin is also known to play a role in tumour metastasis, neoplasia, osteoporosis, Paget's disease, retinopathy, arthritis, periodontal disease, psoriasis and smooth muscle cell migration. Interferon alpha is a family of proteins which possess complex antiviral, antineoplastic and immunomodulating activities. Interferon alpha is effective against a variety of cancers including hairy cell leukaemia, chronic myelogenous
                                                                 They are also useful as antiviral, antifungal and antibacterial agents This sequence is a peptide linker used in the construction of the mult: functional bioconjugates
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 19; Page 88; 123pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             New bioconjugates comprising an avb3 antagonist and a metastatic-
associated receptor ligand, useful for treating cancer and other
anglogenic diseases, or as antiviral, antifungal or antibacterial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             tumour; osteoporosis; Paget's disease; Karposi's sarcoma; periodontal disease; metastasis; neoplasia; retinopathy; arthritis; psoriasis; leukaemia; malignant melanoma; atherosclerosis; smooth muscle cell migration; inhibition; treatment; antagonist; angina;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY83210;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     for treating a human patient with an angiogenesis-mediated disease, e.g. cancer, arthritis, or macular degeneration. The a_vb_3 integrin is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     13-AUG-1998;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              thrombosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    24-JUL-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      peptide or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              restenosis;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          comprising one or more a vb_3 antagonist moieties coupled or polypeptide having anti-angiogenic properties can be use
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 98US-0096442P.
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Matches Query Match

y Match 100.0%; Local Similarity 100.0%; hes 5; Conservative (

Score 28; DB 3; Pred. No. 1.7e+06; No. 1.7e+06; No. 1.7e+06;

Length 5;

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                                                                                                                                               RESULT 12
                                                                                                                                                                                                                                           Query Match
Best Local
                                                                                                                                                                                                                                 Matches
                                                                                                                                                                                                                                                                                                  The present sequence is a peptide which was inserted into expression vector pCANTAB5E to enable more flexible folding of the human eosinophil derived neurotoxin protein (EDN), which was expressed by the vector. This protein can be directed to cancerous cells using additional N-terminal peptides, where it exerts a cytotoxic effect. The protein can, therefore, be used to treat cancer, particularly Kaposi's sarcoma, and to selectively kill neoplastic and non-neoplastic endothelial cells
                                                                                                                                                                                                                                                                                                                                                                                                                        N-terminally modified RNase A targeted to and are cytotoxic to cancerous endothelial cells used to treat especially Kaposi's \alpha
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAB06226 standard; peptide; 5
             Interleukin-12;
IL-12 p40 subuni
                                                 Linker from
                                                                        14-FEB-2000
                                                                                               AAY54917
                                                                                                                                                                                                                                                                              Sequence 5
                                                                                                                                                                                                                                                                                                                                                                                                   Example 9;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Rybak
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Synthetic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Modified RNase; eosinophil derived neurotoxin protein; EDN; cancer; Kaposi's sarcoma; neoplastic endothelial cell;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Expression
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                                                                                                                      AAY54917 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (USSH ) US DEPT HEALTH & HUMAN SERVICES.
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5; Conserv
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lastic endothelial cell; express
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              subunit;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Newton
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                                                                                                                                                                                                                                                                               ξ
                                               IL-12 fusion protein.
                                                                                                                                                                                                                                 Conservative
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                                                                        (first
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            IL-12; fusion protein; IL-12 p35 subunit; B7
it; gene therapy; tumour; leukaemia; linker.
                                                                                                                                                                                                                                                                                                                                                                                                  34; 51pp;
                                                                        entry)
                                                                                                                                                                                                                                          100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                  English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   inserted peptide.
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Pred. No.
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ches 0;
                                                                                                                                                                                                                                                       DB 3;
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                                                                                                                                                                                                                                                     Length 5;
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                        protein;
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CC construct [1] comprising a region encoding an Interleukin-12 (II-12)
CC fusion protein (comprising an II-12 p35 subunit, an II-12 p40 subunit and
CC a linker peptide (joining the subunits) and a region encoding a B7
CC protein. (I) may be used to produce II-12 fision proteins according to
CC standard recombinant DNA methodologies. The fusion proteins may be
CC protein a recombinant DNA methodologies. The fusion proteins may be
CC produced either in vitro in a fermentation culture or in vivo as part of
CC a gene therapy protocol (in this case (I) is used to transform a patients
CC cells, which then secrete the functional polypeptide to supplement the
CC patients own production of II-12 or to rectify mutations which lead to
CC the expression of inactive polypeptides). The fusion proteins produced in
CC this way may be used to treat any disease which responds to II-12 such as
CC and cervical tumours and melanomas) and in particular, tumours of the
CC antigens in the production of antibodies to II-12 and to assay for
CC angonists and antagonists of its activity. The antibodies may be used a
CC diagnostically as a probe which hybridizes to sequences encoding II-12
CC polypeptides in samples. They may be used diagnostically to quantitate
CC the expression of the polypeptide by patients and hence which subjects
CC may be in need of restorative therapy
Sequence 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Nucleic acid constructs encoding interleukin-12 fusion proteins useful for treating leukemia and other cancers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WPI; 2000-038261/03
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-NOV-1996;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         This sequence represents a linker that can be used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Claim 3; Col 93; 73pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    08-NOV-1996;
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밁 Ś Matches Query Match Best Local Similarity AAY43750 standard; peptide; 5 _ 5 GGGGS 5 eeees 5 Conservative 100.0%; Score 28; 1 100.0%; Pred. No. 1 .. Mismatches DB 3; 1 1.7e+06; Length Indels 0 Gaps 0

11-FEB-2000 (first entry)

Linker used to construct a bispecific single-chain antibody.

ARSULT 13
AAY43750
ID AAY43750
AC AAY43
AC AAY43
AC AAY43
AC AAY41
AC AAY41 bscCD19xCD3 antibody; bispecific single-chain fragment; CD19 antigen; CD3 antigen; CD19-positive target cell; T-cell stimulation; cytotoxic T-lymphocyte; B-cell malignancy; myasthenia gravis; B-cell mediated autoimmune disease; Morbus Basedow; Hashimoto thyroiditis; Goodpasture syndrome; B-cell depletion; non-Hodgkin lymphoma; gene therapy; cancer; viral disease.

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence represents a linker used in the construction of CC bispecific single-chain polypeptides of the invention. These polypeptides CC comprise domains providing binding-site of immunoglobulin chains or CC constibutes specifically recognizing CD19 and CD3 antigen. The polypeptide CC destroys CD19-positive target cells without any need of T-cell pre and/or CC co-stimulation, by recruiting cytotoxic T-lymphocytes and so specific CC lysis by T-cells rather than a direct effect by an antibody is achieved. CC are used for the treatment of B-cell malignancies, B-cell mediated CC autoimmune diseases like mysathenia gravis, Morbus Basedow, Hashimoto CC thyroiditis or Goodpasture syndrome or for the depletion of B-cells and CC more particularly non-Hodgkin lymphoma in mammals preferably human. They CC can also delay the pathological conditions caused by these diseases, and CC can be used for detecting these diseases. The polynucleotide is used for can be celly-cell mediated immune response with can in turn be used for treating cancer, its related diseases and also for inhibiting coverably viral diseases by preventing viral infection
                                                                                                                                                                                                                                                                                                                                                                                                                    Query Match
Best Local (
                                                                                                                                                                                                                                                                                                                                                                                                       Matches
                                                                                     HIV-1; gp41; N-helical domain; heptad repeat region; C-helical domain; gp41 transmembrane-proximal amphipathic alpha-helical segment; core 6-helix bundle; viral entry inhibition; immunogenic; antibody; humoral response; broad spectrum vaccine; anti-HIV;
              WO200040616-A1
                                                                        envelope
                                                                                                                                                                                               24-NOV-2000
                                                                                                                                                                                                                                                             AAB14535 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          especially non-Hodgkin lymphoma.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 2000-013241/01
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 10; Page 49; 91pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   21-APR-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                    Similarity
                                                                                                                                                                                                                                                                                                                                                                                                    5
                                                                        glycoprotein; prophylaxis;
                                                                                                                                                                                                                                                                                                                                                                       GGGGS 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AA;
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                                                                                                                                                                                               (first entry)
                                                                                                                                                                 for joining
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   99WO-EP002693
                                                                                                                                                                                                                                                           peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                  100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Bargou R,
                                                                                                                                                                 HIV-1 gp41 N- and C-terminal helices.
                                                                                                                                                                                                                                                             σ
                                                                                                                                                                                                                                                                                                                                                                                                    0,
                                                                                                                                                                                                                                                                                                                                                                                                                  Score 28; DB 3;
Pred. No. 1.7e+06;
                                                                                                                                                                                                                                                                                                                                                                                                    Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         treating B-cell malignancies
                                                                                                                                                                                                                                                                                                                                                                                                  0;
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RESULT 15
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                                                                                                                                                                                                                                                                                                                                                                                                                   Query Match
Best Local S
Matches 5
Fusion protein; HIV; human immunodeficiency virus; antibody; Fv; acquired immune deficiency syndrome; neutralisation; infection; gene therapy; CD4; gplz0; glycoprotein; resistance; vaccination; binding domain; single chain antibody; chimera; chimeric protein.
                                                                                                        Linker used
                                                                                                                                                                                        AAB00156;
                                                                                                                                                                                                                               AAB00156 standard; peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -relevant gp41 structures may also be used therapeutically and to further elucidate the mechanism of HIV cell entry. The press sequence represents a peptide linker which may be used to join of the invention together to form multimers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Raising neutralizing antibody response to human immunodeficiency virus, comprises administering a polypeptide capable of forming a stable coile coil solution structure.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 15; 97pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                08-JAN-1999; 99US-0115404P.
07-JAN-2000; 2000US-00480336.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention relates to raising a neutralising antibody response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               10-JAN-2000; 2000WO-US000456
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  (WILD/) WILD C T. (WEIS/) WEISS C D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           spectrum of HIV
                                                                                                                                                                                                                                                                                                                                                                            1 GGGGS 5
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                                                                                                                                                                                                                                                                                                                                                                                                                                          Similarity
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                                                                                                     in sCD4-SCFv(17b) fusion protein.
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                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                      100.0%;
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Pred. No. 1.7e+06;
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Search completed: November 21, 2004, 13:37:11 Job time : 5.58212 secs
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                                                                                                                                                                                                                                                                            SCD4-SCFv(17b) is a neutralising bispecific fusion protein capable of CC binding to two sites of its target protein. The protein comprises a first CC binding domain capable of binding domain site on the target protein, a second binding domain capable of forming neutralising complex CC with an induced epitope of the target protein and a linker comnecting the CC binding domains. SCD4-SCFv(17b) comprises a soluble CD4 fragment CC (contening domains. D1 and D2) fused to a single chain Fv portion of CC mimetic is used for inactivating gp120 protein of HIV, and for CC neutralising HIV. It is also used for blocking and preventing the binding CC fite viral or recombinant gp120 protein to soluble CD4 or lymphocyte CC fite viral or recombinant gp120 protein to soluble CD4 or lymphocyte CC fite viral or resting HIV replication. The chimeric proteins is CC particularly useful in the prevention of infection during or immediately after HIV exposure (e.g., mother/infant transmission, post-exposure CC prophylaxis, and as a topical inhibitor) and for providing long term CC resistance to HIV infections and AIDS. Gene therapy is used to secrete the bispecific protein at mucosal surfaces, such as the vaginal, rectal CC roal mucosa. The fusion proteins is highly potent, broadly cross-cc mediated undesirable targetting properties. When the fusion protein is substantially derived from human proteins, it has minimal immunogenicity and toxicity in humans which is of great value in prevention of infection of infection of curing or immediately after HIV exposure
                                                                                                                                                                                   Query Match
Best Local Similarity
                                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Novel neutralizing bispecific fusion proteins effective in viral such as HIV neutralization, comprises two different binding domains, inducing-binding domain and induced-binding domain functionally linked by linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic.
                                                                                                                                                                                                                                              Sequence 5 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 2000-638183/61.
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                                                                                 | GGGGS 5
                                                                                                                                                               5; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         99US-0124681P.
                                                                                                                                                           100.0%; Score 28; DB 3; 1
100.0%; Pred. No. 1.7e+06;
tive 0; Mismatches 0;
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92

Sequence:

Perfect score:

Scoring table:

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340, Appl 124, Appl 124, Appl 3, Appli 62, Appli 5, Appli 5, Appli 5, Appli 64, Appli 64, Appli 64, Appli 64, Appli 64, Appli 62, Appli 62, Appli 62, Appli 62, Appli

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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
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seq length: 2000000000
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Match Length
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1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/FCTUS_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd
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US-08-25-224-54
US-08-236-918A-18
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US-08-236-918A-18
US-08-236-31-140
US-08-236-33-577-6
US-08-575-341A-32
US-08-575-361A-32
US-08-677-1939-140
US-08-471-939-140
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US-08-685-782-75
US-08-871-068-140
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US-08-903-668-130
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                                              ; MOLECULE TYPE: protein US-07-959-946-6
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US-07-959-946-6
                                                                                                                                                                                        MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/959,946
FILING DATE: 19921008
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/901,706
FILING DATE: 18-JUN-1992
ATTORNEY/AGENT INFORMATION:
NAME: Gammon, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sequence 6, Application US/07959946 Patent No. 5408038
Query Match
Best Local Similarity
                                                                                                                                               TELEPHONE: (312)616-5400
TELEFAX: (312)616-5460
INFORMATION FOR SEQ ID NO: 6
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
TYPE: AMINO ACID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: Koduri, Raju
APPLICANT: Young, Stephen G.
APPLICANT: Witztum, Joseph L.
APPLICANT: Curtiss, Linda K.
TITLE OF INVENTION: Lipoprotein Assays Using Antibodies to a
TITLE OF INVENTION: Pan Native Epitope and Recombinant Antigens
NUMBER OF SEQUENCES: 20
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 60601
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Smith, Richard
APPLICANT: Koduri, Raju
APPLICANT: Young, Stephen
APPLICANT: Witztum, Joseph
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
                                                                             TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Dressler, Goldsmith, Shore, Sutker ADDRESSEE: Milnamow, Ltd.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  180 No. 5408038th Stetson, Suite 4700
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US-08-776-271-3
US-08-621-859-64
US-09-100-856A-62
US-09-046-992-5
US-09-075-511-64
US-09-091-51-64
US-09-091-51-64
US-09-091-61-62
US-09-0818-252-40
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DB 1; 3.8e+05;

Length

Result

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Score

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RESULT 3
US-08-471-052A-140
US-08-471-052A-140
; Sequence 140, Application US/08471052A
; Patent No. 5625033
; Patent No. 562503.
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TELEX: 66141 PENNIE
INFORMATION FOR SEQ ID NO: 140
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/08
PILING DATE:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: MARGE COLUMN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/08/176 FOLIAGE DATE: CLASSITETED NUMBER: US/08/176 FOLIAGE DATE: US/08/176 FOLIAGE 
                                                                                                APPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 166
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC-DOS/MS-DOS
COPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Kay, B. K.
APPLICANT: Fowlkes, D. M.
TITLE OF INVENTION: Totally Synthetic Affinity Reagents
NUMBER OF SEQUENCES: 141
                                CORRESPONDENCE ADDRESS:
ADDRESSEE: Pennie & Edmonds
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SEQUENCE CHARACTERISTICS:
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ADDRESSEE: Pennie &
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     <u>ب</u>
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1155 Avenue of the Americas
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100.0%; Pative 0;
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Pred. No. 3.8e+05;
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; MOLECULE TYPE: peptide US-08-471-052A-140
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SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino ~ ''
Type
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
OPERATION NUMBER: US/08/471,052A
FILING DATE: 06-JUNE-1995
CLASSIFICATION: 530
ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
THE PROPERTY NUMBER: 18,872
                                                                                                                                                                                   ZIP: 94105-1493
COMPUTER READABLE FORM:
MEDDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/225,224
FILING DATE: 8-APR-1994
CLASSIFICATION: 530
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              GENERAL INFORMATION
                 ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
REGISTRATION UNMBER: 32,762
REFERENCE/DOCKET NUMBER: 1528
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 543-9600
TELEPAX: (415) 543-5043
NFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES: 57
CORRESPONDENCE ADDRESS:
CORRESPONDENCE TOWNSEND AND TOWNSEND Khourie and Crew STREET: Steuart Street Tower, One Market Plaza CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: PASTAN, IRA
APPLICANT: KREITMAN, ROBERT J.
TITLE OF INVENTION: CIRCULARLY PERMUTATED LIGANDS AND
TITLE OF INVENTION: CIRCULARLY PERMUTED FUSION PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE/DOCKET NUMBER: 11
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEPAX: 212 869-8864/9741
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                                                                                             15280-193
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RESULT 6
US-08-463-163-1
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Best Local Similarity
Matches 5; Conserv
                                                                                                                                         Matches
                                                                                                                                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: Apple Power Macintosh

COMPUTER: Apple Power Macintosh

OPERATING SYSTEM: Apple 7.5.3

SOFTWARE: Microsoft Word, Version #6.0.1

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/236,918A

FILING DATE: 06-May-1994

CLASSIFICATION 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 08/060,843

FILING DATE: 07-May-1993

CLASSIFICATION. 435

PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Patent No.
                                                                                                                                                                                                              -08-236-918A-18
                                                                                                                                                                                                                                                                                                                  TELEFAX: (206) 233-06
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                     TELECOMMUNICATION INFORMATION: TELEPHONE: (206) 587-0430
                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Alderson, Mark R.
APPLICANT: Goodwin, Raymond G.
APPLICANT: Smith, Craig A.
TITLE OF INVENTION: Cytokine Designated 4-1BB Ligand
NUMBER OF SEQUENCES: 18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: unknown MOLECULE TYPE: peptide
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                                                                                                                                                                                                                             MOLECULE TYPE: peptide
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                                                                                                                                       Local Similarity nes 5; Conserv
                                                                                                                                                                                                                                                                                                                                                                                        NAME: Anderson, Kathryn A.
REGISTRATION NUMBER: 32,172
REFERENCE/DOCKET NUMBER: 2801-B
                                                                                                                                                                                                                                               TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CITY: Seattle
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                                                                                                                                                       100.0%; Score 28; DB 1; 100.0%; Pred. No. 3.8e+05;
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                                                                                                                                         Mismatches
                                                                                                                                                                        Length 5;
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US-08-566-800A-58
US-08-566-800A-58
; Sequence 58, Application US/08566800A
; Patent No. 5736364
; GENERAL INFORMATION:
APPLICANT: Kelley, Robert F.
APPLICANT: Lezarus, Robert A.
APPLICANT: Lee, Geoffrey F.
APPLICANT: Lee, Geoffrey F.
TITLE OF INVESTION: No. 5736364el Factor VIIa Inhibitors
; TITLE OF SEQUENCES: 58
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/463,163
FILING DATE: 05-UN-1995
CLASSIFICATION DATA:
APPLICATION NUMBER: US 06/227,227
FILING DATE: 22-JAN-1981
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 06/911,227
FILING DATE: 24-SEP-1986
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,361
FILING DATE: 21-APR-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,361
FILING DATE: 21-APR-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,361
FILING DATE: 01-APR-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/341,361
FILING DATE: 01-APR-1999
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/865,722
FILING DATE: 08-APR-1992
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Ellen L.
BRGITSTBATTON NUMBER: 13-762
                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity
Matches 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: (415) 543-50
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY: linear MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: FitzGerald, David J
APPLICANT: Chaudhary, Vijay K.
APPLICANT: Pasten, Ira H.
APPLICANT: Waldmann, Thomas A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Queen, Cary L. TITLE OF INVENTION: Recom
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         REGISTRATION NUMBER: 32
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CITY: San Francisco
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Pred. No. 3.8e+05;
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CORRESPONDENCE ADDRESS:

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Best Local Similarity lov.
"--- hes 5; Conservative
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MEDIUM TYPE: 3.5 inch, 1.44 Mb floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WinPatin (Genentech)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/566,800A
FILING DATE: 04-Dec-1995
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 415/952-9881
TELEX: 910/371-7168
INFORMATION FOR SEQ ID NO:
                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/244,469
FILING DATE: 01-UN-1994
CLASSIFICATION: 514
CLASSIFICATION: 514
                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Paul, Ralph W.
APPLICANT: Overell, Robert
TITLE OF INVENTION: ENVELOPE FUSION VECTORS FOR USE IN GENE
TITLE OF INVENTION: DELIVERY
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS: ADDRESS: MORRISON & FOERSTER
STREET: 755 PAGE MILL ROAD
CITY: PALO ALTO
STATE: CA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acids
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REGISTRATION NUMBER: 36,575
REFERENCE/DOCKET NUMBER: POS
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415/225-8228
ATTORNEY/AGENT INFORMATION:
NAME: Dylan, Tyler M.
REGISTRATION NUMBER: 37,612
REFERENCE/DOCKET NUMBER: 22627-20007.20
TELECOMMUNICATION INFORMATION:
TELEPHONE: (415) 813-5600
                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Genentech, Inc.
STREET: 460 Point San Bruno Blvd
CITY: South San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                   COUNTRY: USA
ZIP: 94304-1018
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TYPE: Amino Acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COUNTRY:
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100.0%; Pred. No. 3.8e+05;
vative 0; Mismatches 0;
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RESULT 10 US-08-333-577-6

Sequence 6, Application US/08333577 Patent No. 5786206

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                                                                                                                                       US-08-189-331-140
                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: Misrock, S. Leslie
REGISTRATION NUMBER: 18,872
REFERENCE/DOCKET NUMBER: 1101-155
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212 790-9090
TELEFAX: 212 869-8864/9741
TELEX: 6614 PENNIE
INFORMATION FOR SEQ ID NO: 140:
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Matches
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Patent No. 5747334
                                                                  Matches
                                                                                                   Query Match
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LENGTH: 5 amino acids
TYPE: amino acid
STRANDERNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEX: 706141 MRSNFOERS SFO INFORMATION FOR SEQ ID NO: 5:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION
                                                                                                                                                 LENGTH: 5 amino acids
TYPE: amino acid
STRANDENDESS: single
TOPOLOGY: unknown
MOLECULE TYPE: peptide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM FORMATION
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              STREET: LIVER YORK CITY: New York STATE: New York CONTRY: U.S.A.
                                                                                                                                                                                                                        SEQUENCE CHARACTERISTICS
LENGTH: 5 amino acids
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: Kay, B. A.
APPLICANT: Fowlkes, D. M.
APPLICANT: Fowlkes, D. M.
TOUGHLY Synthetic Affinity Reagents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
                                                               Local Similarity hes 5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DDRESSEE:
                                  1 GGGGS 5
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                                                                    Conservative
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                                                                                  100.0%; Score 28; DB 1; 100.0%; Pred. No. 3.8e+05;
                                                                    <u>..</u>
                                                                    Mismatches
                                                                                                    Length 5;
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SENERAL INFORMATION:

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US-08-575-361A-32
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LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-333-577-6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.0%; Score 28; DB 1; Best Local Similarity 100.0%; Pred. No. 3.8e+05; Matches 5; Conservative 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                      Sequence 32, Application US/08575361A Patent No. 5792640
                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (312)616-546
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ATTORNEY/AGENT INFORMATION:
NAME: Gameon, Edward P.
REGISTRATION NUMBER: 29,381
REFERENCE/DOCKET NUMBER: SCRP
TELECOMMUNICATION INFORMATION:
TELEPHONE: (312)616-5400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT:
APPLICANT:
ZIP: 20005-3918
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Re-lease #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: FORDPY disk
COMPUTER: IBM PC compatible
COMPUTER: FOR PC LOOS/MS-DOS
SOFTMARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UMBER: US/08/333,577
FILING DATE:
CLASSIFICATION: 530
CLASSIFICATION: 530
                                                                                                                                                                                                                                                                               TITLE OF INVENTION:
TITLE OF INVENTION:
NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: Witztum, Joseph L.
APPLICANT: Curtiss, Linda K.
TITLE OF INVENTION: Lipoprotei
TITLE OF INVENTION: Pan Native
                                                                                                                                                                                                                                                                  CORRESPONDENCE ADDRESS
                                                                                                                                                                                                                                                                                                                                                    APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STATE: I
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CITY: Chicago
STATE: Illinois
                                                                                                                                                                                                         STREET:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Dressler, Goldsmith, Shore, Sutker & ADDRESSEE: Milnamow, Ltd.
                                                                                                                                          COUNTRY:
                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 6060:
                                                                                                                                                                                  Washington
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                                                                                                                                                                                                           Tower
                                                                                                                                                                                                                        E: Cushman Darby & Cushman L.L.P.
1100 New York Avenue, NW, Ninth Floor, East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             180 No. 5786206th Stetson, Suite 4700
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             : (312) 616-5460
(312) 616-5460
777 TD NO: 6:
                                                                                                                                                                                                                                                                                   Chandrasegaran, Srinivasan
VENTION: A GENERAL METHOD TO CLONE HYBRID
VENTION: RESTRICTION ENDONUCLEASES USING lig GENE
EQUENCES: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    USA
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Young, Stephen G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Richard K.
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Query Match
Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence
                                                                                                                                                                                    APPLICATION NUMBER: US/08/564,955
FILING DATE: 30-NOV-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/198,431
FILING DATE: 17-FEB-1994
PRIOR APPLICATION NUMBER: US 08/537,874
FILING DATE: 30-OCT-1995
PRIOR APPLICATION DATA:
APPLICATION DATA:
                                  APPLICATION NUMBER: PCT/US95/
FILING DATE: 17-FEB-1995
ATTORNEY/AGENT INFORMATION:
NAME: DUNN, TRACY J.
REGISTRATION NUMBER: 34,587
REFERENCE/DOCKET NUMBER: 1652
TELECOMMUNICATION INFORMATION:
TELEDHONE: (415) 326-2400
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEX: 6714627 CUSH
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
TELEFAX: (415) 576-03
INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TITLE OF INVENTION: METT TITLE OF INVENTION: HAV TITLE OF INVENTION: RECONDRESS OF SEQUENCES: 67 CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: STEMMER, WILLEM P.C.
APPLICANT: CRAWERI, ANDREAS M.
TITLE OF INVENTION: METHODS FOR GENERATING POLYNUCLEOTIDES
TITLE OF INVENTION: HAVING DESIRED CHARACTERISTICS BY ITERATIVE SELECTION AND
TITLE OF INVENTION: RECOMBINATION
                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARB: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: U.S.A.
ZIP: 94111-3834
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELECOMMUNICATION INFORMATION: TELEPHONE: 202-861-3000
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        TELEPHONE: (415)
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TELEFAX: 202-822-0944
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME: Kokulis, Paul N. REGISTRATION NUMBER: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 5 amino acids
TYPE: amino acid
TOPOLOGY: linear
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          T: TWO EMBARCADERO CENTER, 8TH FLOOR SAN FRANCISCO
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              576-0300
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Pred. No. 3.8e+05;
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                                                                                                                       US-08-528-523-13
                                                                                                                                                                                                         TELEX: 64191
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 5 amino acide
TYPE: amino acid
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Patent No. 58247
                                                            Matches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Query Match 100.0%;
Best Local Similarity 100.0%;
Matches 5; Conservative 0
                                                                                         Query Match
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                                                                                                                                                                                                                                                                                                                                  FILING DATE: 16-SEP-1994
ATTORNEY/AGENT INFORMATION:
NAME: Hamlet-King, Diana
REGISTRATION NUMBER: 33,302
REFERENCE/DOCKET NUMBER: Mei
                                                                                                                                      HYPOTHETICAL: FRAGMENT TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                             CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/0
FILING DATE: 06-NOV-1992
CLASSIFICATION: 536
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                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                        TELECOMMUNICATION INFORMATION: TELEPHONE: 703-243-6333
                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 94114572.4
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CORRESPONDENCE ADDRESS:
                                                           Local Similarity hes 5; Conserv
                                                                                                                                                                                                                                                                               TELEPHONE: 703-243-6410
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
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STATE: Virginia
COUNTRY: U.S.A.
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STRANDEDNESS: si
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                                                                                                                                                                                               STRANDEDNESS: single
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T: Matzku, Siegfried
INVENTION: Immunoconjuga
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                                                            Conservative
                                                                                                                                                                                    linear
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                                                       Score 28; DB 2; I
Pred. No. 3.8e+05;
; Mismatches 0;
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RESULT 14

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                                                                                                                                                                                                                                                                                                              Sequence 86,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Matches
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                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Hollig
APPLICANT: Griffi
                                                                                                                                                                          APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP PCT/US95/0:
FILING DATE: 17-FEB-1995
APPLICATION NUMBER: US 08/198,431
FILING DATE: 17-FEB-1994
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME: Liebeschuetz, Joe
REGISTRATION NUMBER: 37,505
REFERENCE/DOCKET NUMBER: 018097-014610
TELECOMMUNICATION INFORMATION:
TELEPHONE: 415-576-0200
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                    APPLICANT: Pope, Anthony R
APPLICANT: Prospero, Terence D
APPLICANT: Winter, Gregory P
TITLE OF INVENTION: Multivalent and Multispecific Binding
TITLE OF INVENTION: Proteins, Their Manufacture and Use
NUMBER OF SEQUENCES: 106
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, 8th Floor
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APPLICANT: Crameri, Andreas
TITLE OF INVENTION: DIA Mutagenesis by Random Fragmentation
TITLE OF INVENTION: and Reassembly
                                                                                                                                                          APPLICANT:
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les 5; Conserv
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CLASSIFICATION: 435
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STATE: CA
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    ADDRESSEE:
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5837242
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Malmqvist, Magnus
Marks, James D
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                                                                                                                                                      McGuinness, Brian T
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    not relevant
Marshall O'Toole Gerstein Murray and Borun
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Pred. No. 3.8e+05;
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CURRENT APPLICATION NUMBER: US/08/448,418

PILING DATE: 14-MAY-1996

CLASSIFICATION: C12N 15/62, 15/70, C07K 1/00

PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/GB93/02492

PILING DATE: 03-DEC-1993

PRIOR APPLICATION NUMBER: GB 9225453.1

FILING DATE: 04-DEC-1992

PRIOR APPLICATION NUMBER: GB 9300816.7

PILING DATE: 16-JAN-1993

PRIOR APPLICATION NUMBER: GB 9300816.7

PILING DATE: 16-JAN-1993

PRIOR APPLICATION NUMBER: GB 9300814.7

PILING DATE: 10-MAY-1993

PRIOR APPLICATION NUMBER: GB 9303614.7

PILING DATE: 10-MAY-1993

PRIOR APPLICATION NUMBER: GB 9319969.3

APPLICATION NUMBER: GB 931969.3

APPLICATION NUMBER: GB 9300816.7

APPLICATIO
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Search completed: November 21, 2004, 13:44:43 Job time: 1.64781 secs
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                                                                                                                                                                                                                                                                                                                                                           Query Match 100.0%; Score 28; DB 2; Length 5; Best Local Similarity 100.0%; Pred. No. 3.8e+05; Matches 5; Conservative 0; Mismatches 0; Indels
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CITY: Chicago
STATE: Illinois
COUNTRY: USA
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
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Result
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Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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Perfect score:
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                                                                                                                                                                                                                                                                                                                                                         Score
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1: /cgn2_6/ptodata/2/pubpaa/USO7_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT NEW PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/USO6_NEW PUB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/USO6_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/USO7_NEW PUB.pep:*

6: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*

7: /cgn2_6/ptodata/2/pubpaa/USO8_NEW PUB.pep:*

8: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*

9: /cgn2_6/ptodata/2/pubpaa/USO8_PUBCOMB.pep:*
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Match Length
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/ Cgm2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
/ Cgm2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
/ Cgm2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
/ Cgm2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
/ Cgm2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
/ Cgm2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
/ Cgm2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
/ Cgm2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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/ Cgm2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
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                              US-09-832-297A-1
US-09-832-297A-2
US-09-287-849-44
US-09-147-142-31
US-09-214-645-1
US-09-719-233-45
US-09-719-233-45
US-09-988-789-3
US-09-988-787-21
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44, Appli
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31, Appli
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ALIGNMENTS

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15,	Sequence 3, Appli	е 37,	e 61,	•	Φ	e 84,	23,	ω •	8	Ø	ce 212	Sequence 2, Appli	Sequence 1, Appli	e 40,	e 8	e 8,	e 56,	æ	e 14,	Sequence 3, Appli	e 123	Sequence 6, Appli	e 10,	e 22,	e u	Sequence 10, Appl	e 25,	e 8,	7,	Sequence 5, Appli	116,

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Sequence 1, Application US/09832297A

Publication No. US20010055566A1

GENERAL INFORMATION:
APPLICANT: FluoroProbe, Inc.
APPLICANT: FluoroProbe, Inc.
TITLE OF INVENTION: METHOD FOR VIEWING TUMOR TISSUE LOCATED WITHIN A BODY CAVITY
FILE REFERENCE: FLUOR1120-2
CURRENT APPLICATION NUMBER: US/09/832,297A
CURRENT FILING DATE: 2001-04-09
PRIOR APPLICATION NUMBER: US 09/362,805
PRIOR APPLICATION NUMBER: US 09/362,805
PRIOR APPLICATION NUMBER: US 09/373,190
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1998-10-15
NUMBER OF SEQ ID NOS: 12
SOFTWARE: PatentIn version 3.1
SEQ ID NO 1
LENGTH: 5
LENGTH: 5
TYPE: PRI
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                                      S
                                                                                                                                                                         ; FEATURE:
; OTHER INFORMATION: Peptide linker moiety
US-09-832-297A-1
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                                                                                     Matches
                                                                                                                              Query Match
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                                                                                                          Local
                                        1 GGGGS 5
                                                                                   Similarity 5; Conserv
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                                                                                 100.0%; Score 28; DB 9; 1
100:0%; Pred. No. 1.4e+06;
Live 0; Mismatches 0;
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RESULT 2 US-09-832-297A-2

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; OTHER INFORMATION: Peptide linker moiety. The sequence can ; OTHER INFORMATION: times where n is a natural number. US-09-832-297A-2
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Query Match
Best Local Similarity
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                                                                                                US-09-287-849-44
                                                                                                                                                                                                                                                                                                                                                                    CURRENT APPLICATION NUMBER: US/09/287,849
CURRENT FILING DATE: 199-04-07
PRIOR APPLICATION NUMBER: US 08/818,112
PRIOR FILING DATE: 1997-03-13
PRIOR APPLICATION NUMBER: US 08/942,578
PRIOR FILING DATE: 1997-10-01
PRIOR APPLICATION NUMBER: US 09/025,197
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/832,297A CURRENT FILING DATE: 2001-04-09 PRIOR APPLICATION NUMBER: US 09/362,805 PRIOR FILING DATE: 1999-07-28 PRIOR APPLICATION NUMBER: US 09/173,190 PRIOR FILING DATE: 1998-10-15 NUMBER OF SEQ ID NOS: 12 SOFTWARE: Patentin version 3.1
                                                                                                                                                                                                                                                                                          PRIOR APPLICATION NUMBER: PRIOR FILING DATE: 1998-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Dillon, Davin C.
APPLICANT: Alderson, Mark
APPLICANT: Campos-Neto, Antonio
APPLICANT: Corixa Corporation
TITLE OF INVENTION: Fusion Protiens of Mycobacterium tuberculosis Antigens
TITLE OF INVENTION: and Their Uses
FILE REFERENCE: 014058-009020US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Fluoroprobe, Inc.
APPLICANT: LUIKEN, GEORGE A.
TITLE OF INVENTION: METHOD FOR VIEWING TUMOR TISSUE LOCATED WITHIN A BODY CAVITY
FILE REFERENCE: FLUOR1120-2
                                                                                                                                                                                                                                                         SOFTWARE:
                                                                                                                                                                                                                                                                          NUMBER OF SEQ ID NOS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: PRT ORGANISM: Artificial sequence
                                                                                                                 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                                        ORGANISM: Artificial Sequence FEATURE:
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Dillon, Davin C.
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                                                                                                                 Description polylinker
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tive 0;
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Pred. No. 1,4e+06;
                Score 28; DB 9; I
Pred. No. 1.4e+06;
; Mismatches 0;
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US-09-147-142-31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ; OTHER INFORMATION: Description of Artificial Sequence: peptide linker US-09-147-142-31
                                                                                                                  US-09-214-645-1
                                      Query Match
Best Local S
Matches 5
                                                                                                                                                                                                                               CURRENT APPLICATION NUMBER: US/09/214,645
CURRENT FILING DATE: 199-09-27
PRIOR APPLICATION NUMBER: PCT/US97/12239
PRIOR FILING DATE: 1997-07-09
NUMBER OF SEQ ID NOS: 13
SOFTWARE: PastSEQ for Windows Version 4.0
SEQ ID NO 1
                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Short, Jay
TITLE OF INVENTION: N
TITLE OF INVENTION: 1
TITLE OF INVENTION: 1
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NUMBER OF SEQ ID NOS: 32
SOFTWARE: PATENTIN VEY: 2.0
SEQ ID NO 31
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: HUDSON, Peter John
APPLICANT: KORTT, Alex Andrew
APPLICANT: IRVING, Robert Alexander
APPLICANT: ATWELL, John Leslie
TITLE OF INVENTION: HIGH AVIDITY POLYVALENT AND POLYSPECIFIC REAGENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    FILE REFERENCE: 016786/0212
CURRENT APPLICATION NUMBER: US/09/147,142
CURRENT FILING DATE: 1999-03-05
EARLIER APPLICATION NUMBER: PCT/AU98/00212
EARLIER FILING DATE: 1998-03-26
EARLIER APPLICATION NUMBER: AU PO 5917
                                                                                                                                                                                                                                                                                                                                                                       FILE REFERENCE:
                                                                                                                                                            TYPE: PRT
ORGANISM: Artificial Sequence
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                                                                                                                                    OTHER INFORMATION: linker peptide
                                                                                                                                                      FEATURE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                Short, Jay M.
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ilarity 100.0%;
Conservative 0
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                                                                                                                                                                                                                                                                                                                                                                                     METHOD OF DNA SHUFFLING WITH POLYNUCLEOTIDES PRODUCED BY BLOCKING OR INTERRUPTING SYNTHESIS OR AMPLIFICATION PROCESS
                                                        100.0%; Score 28; DB 9; 100.0%; Pred. No. 1.4e+06;
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Pred. No.
                                        Mismatches
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GGGGS

US-09-858-616-2

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GENERAL INFORMATION:
APPLICANT: Case, Casey
ITITLE OF INVENTION: CELLS FOR DRUG DISCOVERY
FILE REFERENCE: 8325-0010
CURRENT APPLICATION NUMBER: US/09/779,233
CURRENT FILING DATE: 2001-02-08
NUMBER OF SEQ ID NOS: 45
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        RESULT 7
US-09-779-233-45
; Sequence 45, Application US/09779233
; Patent No. US20020045158A1
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Best Local Similarity
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RESULT 8
US-09-989-789-3
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                                                                                                                                                                                                                      ; OTHER INFORMATION: Description of Artificial Sequence: linker US-09-779-233-45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PRIOR APPLICATION NUMBER: US 09/571,499
PRIOR FILING DATE: 2000-05-15
PRIOR APPLICATION NUMBER: US 09/557,276
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APPLICANT: SHORT, Jay
TITLE OF INVENTION: SEQUENCE BASED SCREENING
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NUMBER OF SEQ ID NOS: 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 PRIOR APPLICATION NUMBER: US 60/008,317
PRIOR FILING DATE: 1995-12-07
PRIOR APPLICATION NUMBER: US 08/944,795
PRIOR FILING DATE: 1997-10-06
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR FILING DATE: 2000-04-24
PRIOR APPLICATION NUMBER: US 08/692,002
PRIOR FILING DATE: 1996-08-02
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CURRENT APPLICATION NUMBER: US/09/858,616
CURRENT FILING DATE: 2001-09-10
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                                                                                                                                                                                                                                                       LENGTH: 5
TYPE: PRT
ORGANISM: Artificial Sequence
PEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ORGANISM: Artificial sequence FEATURE: OTHER INFORMATION: Linker peptide
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                                                                       GGGGS 5
                                                                                                                                            100.0%; Score 28; DB 9; ilarity 100.0%; Pred. No. 1.4e+06; Conservative 0; Mismatches 0;
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US-09-192-854-180

Sequence 180, Application US/09192854

Patent No. US20020068276A1

GENERAL INFORMATION:
APPLICANT: Winter, Greg
APPLICANT: Tomlineon, Ian
TITLE OF INVENTION: Methods for Selecting Functional Peptides
FILE REFERENCE: 3789/72916

CURRENT APPLICATION NUMBER: US/09/192,854

CURRENT FILING DATE: 1998-11-17
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; OTHER INFORMATION: Description of Artificial Sequence: peptide linker
US-09-989-789-3
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Best Local Similarity
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SEQ ID NO 3
LENGTH: 5
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APPLICANT: Witte, Larry
TITLE OF INVENTION: Antibodies Specific to KDR and Uses Thereof
FILE REFERENCE: 11245/46505
CURRENT APPLICATION NUMBER: US/09/976,787
CURRENT FILING DATE: 2001-10-12
PRIOR APPLICATION NUMBER: US 09/493,539
PRIOR FILING DATE: 2000-01-28
PRIOR FILING DATE: 2000-01-28
PRIOR APPLICATION NUMBER: US 60/117,726
PRIOR FILING DATE: 1999-01-29
PRIOR FILING DATE: 1999-01-29
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Best Local Similarity
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CURRENT FILING DATE: 2002-03-25
NUMBER OF SEQ ID NOS: 4085
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FILE REFERENCE: 8325-0011.20 / S11-US2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      APPLICANT: LIU, Qiang
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                                                                                                                                                                                                                                                                                                                                                                                                                                                             OTHER INFORMATION: peptide linker
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Pred. No. 1.4e+06;
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RESULT 12
US-09-333-527-5
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US-09-761-962-36
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Patent No. US20020077285A1
GENERAL INFORMATION:
APPLICANT: Memorial Sloan-Kettering Cancer Center
TITLE OF INVENTION: Identification and Characterization
TITLE OF INVENTION: Variants of Mu-
TITLE OF INVENTION: opioid Receptor (MOR-1) Gene
FILE REPERENCE: 830002-2000.1
CURRENT APPLICATION NUMBER: US/09/761,962
CURRENT FILING DATE: 2001-01-17
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PRIOR FILING DATE: 2001-03-13
NUMBER OF SEQ ID NOS: 46
SOFTWARE: Patentin version 3.0
SEQ ID NO 36
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Patent No. US20020078472A1
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Best Local Similarity
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EARLIER FILING DATE: 1997-11-21
NUMBER OF SEQ ID NOS: 212
SOFTWARE: Patentin Ver. 2.0
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ORGANISM: Homo sapiens
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               COMPUTER READABLE FORM: MEDIUM TYPE: Diskette,
                                                                                                                                                                                                    APPLICANT: Paul CHRISTOU; EVA STROGER; Rainer FISCHER; Carmen MARTIN-VAQUERO; Stef
                                                                                                                                                              NUMBER OF SEQUENCES: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local Similarity
nes 5; Conservat
                                                                                      ADDRESSEE: Fulbright & Jaworski L.L.P. STREET: 666 Fifth Avenue CITY: New York City
STATE: New York
COMPUTER:
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IBM PS/2
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Query Match
Best Local Similarity
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RESULT 14
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APPLICANT: Zhang, Lei

APPLICANT: Zhang, Lei

TITLE OF INVENTION: Functional Genomics Usir

FILE REFERENCE: 019496-002000US

CURRENT APPLICATION NUMBER: US/09/925,796

CURRENT FILING DATE: 2001-08-09

PRIOR APPLICATION NUMBER: 09/395,448

PRIOR FILING DATE: 1999-09-14
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Best Local S
Matches 5
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PRIOR FILING DATE: 1999-01-12
NUMBER OF SEQ ID NOS: 23
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 8
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INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                           TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                              FEATURE:
                                                                                                                                                                                                                                                                                 LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REGISTRATION NUMBER: 36,669
REFERENCE/DOCKET NUMBER: KL/JIC 202.1 -
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 318-3000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: 60/08: FILING DATE: June 15, 1998 ATTORNEY/AGENT INFORMATION: NAME: Mary Anne Schofield
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CURRENT APPLICATION DATA:
APPLICATION NUMBER: US,
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                                                                                                                                                      Length 5;
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US-09-815-837-116
Sequence 116, Application US/09815837
Patent No. US20020082411A1
GENERAL INFORMATION:

APPLICANT: Carter, Darrick

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GENERAL INFORMATION: GENERALIANT: GENERAL INFORMATION: Shai

APPLICANT: Warkoni, Shai

APPLICANT: Ben-Yehudah, Ahmi

APPLICANT: Acar, Yehudith

APPLICANT: Aqeilan, Rami

APPLICANT: Lorberboum-Galski, Haya

APPLICANT: Lorberboum-Galski, Haya

APPLICANT: Lorberboum-Galski, Haya

APPLICANT: Lorberboum-Galski, Haya

APPLICANT: Beloctstocky, Ruth

APPLICANT: Beloctstocky, Ruth

APPLICANT: Beloctstocky, Ruth

APPLICANT: Beloctstocky, Ruth

APPLICANT: Coldent MITH CELL-TARGETING

TITLE OF INVENTION: SPECIFICITY AND APOPTOSIS-INDUCING ACTIVITIES

FILE REFERENCE: 9457-009-999

CURRENT FILING DATE: 1998-03-02

NUMBER OF SEQ ID NOSHOWS PRICE OF SEQ ID NOSHOWS PRICE OF SEQ ID NOSHOWS PRICE ORGANISM: Artificial Sequence

FEATURE:

OTHER INFORMATION: Flexible polylinker

US-09-033-525-5
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ITITLE OF INVENTION: Immune Medators and Related Methods
FILE REFERENCE: 014058-005670US
FILE REFERENCE: 014058-005670US
CURRENT APPLICATION NUMBER: US/09/815,837
CURRENT FILING DATE: 2001-03-22
PRIOR APPLICATION NUMBER: US 60/204,249
PRIOR FILING DATE: 2000-03-22
PRIOR FILING DATE: 2000-05-15
PRIOR APPLICATION NUMBER: US 60/264,003
PRIOR FILING DATE: 2001-01-23
NUMBER OF SEQ ID NOS: 129
SOFTWARE: Patentin Ver. 2.1
SEQ ID NO 116
LENGTH: 5
CORGANISM: Artificial Sequence
PEATURE:
OTHER INFORMATION: Description of Artificial Sequence:downstream
OTHER INFORMATION: linker for CO596
Search completed: November 21, 2004, 14:03:48 Job time: 3.18978 secs
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Best Local Similarity
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Patent No. US20020090374A1
GENERAL INFORMATION:
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Local Similarity 100.0%; Pred. No. 1.4e+06;
les 5; Conservative 0; Mismatches 0; Indels
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RESULT 2 A86333 hypothetical protein (Species: Arabidope C;Date: 02-Mar-2001 C;Accession: A86333 R;Theologis, A.; Edi Chin, C.W.; Chung, ansen, N.F.; Hughes, Nature 408, 816-820, A;Authors: Hunter, C.A.; Li, U.H.; Li, Rizzo, M.; Rooney, C.A.; Li, WH. D.; Yu, A;Title: Sequence and, Reference number: A;Accession: A86333 A;Status: preliminal A;Molecule type: DNA A;Cross-references: C;Genetics: C;Geneti	Query Match Best Local Matches Qy 1	RESULT 1 System of the state of		0 1 2 2 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4 4
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ana I #text_change 09-Jul-2004 iel, N.A.; Kaul, S.; White, O.; Alonso, Conway, A.R.; Creasy, T.H.; Dewar, K.; Sson, C.; Khan, S.; Khaykin, E.; Kim, C. Z.A.; Luros, J.S.; Maiti, R.; Marziali, P.; Southwick, A.M.; Sun, H.; Tallon, C.; Davis, R.W. the plant Arabidopsis. 1130712 NID:98779001; PIDN:AAF79916.1; GSPDB:GN	Length 37; 12; 0; Indels 0; Gaps 0;	#text_change 09-Jul-2004 #text_change 09-Jul-2004 Stericin homologue from Sarcophaga per		hypothetical prote globulin 2 precurs hypothetical prote hypothetical prote hypothetical prote hypothetical prote glycine-rich prote glycine-rich prote probable gas vesic glycine-rich prote probable glycine-rich prote probable prote probable prote protect protect hypothetical prote hypothetical prote hypothetical prote sTIG1 protein hypothetical prote sylpothetical prote

Query Match Best Local Similarity

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Score 28; DB 2; Length 64; Pred. No. 2.2e+02;

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R;Davagnino, J.; Herrero, M.; Furlong, D.; Moreno, F.; Kolter, R.
Proteins 1, 230-238, 1986
A;Title: The DNA replication inhibitor microcin B17 is a forty-three-amino-acid protein
A;Reference number: A25219; MUID:88217867; PMID:3329729
A;Accession: A25219
A;Accession: A25219
A;Accession: Cype: DNA
A;Molecule type: DNA
A;Residues: 1-69 < DAV>
A;Cross-references: UNIPROT:P05834; GB:M15469; NID:g146787; PIDN:AAA24141.1; PID:g146788
A;Cross-references: UNIPROT:P05834; GB:M15469; NID:g146787; PIDN:AAA24141.1; PID:g146788
R;Genilloud, O; Moreno, F.; Kolter, R.
U. Bacteriol. 171, 1126-1135, 1989
                                                                                    A; Molecule type: DNA, A; Residues: 1-14 <CON.
A; Residues: 1-14 <CON.
A; Cross-references: EMBL: X06417; NID: g41978; PIDN: CAA29725.1; PID: g41979
R; Li, Y.M.; Milne, J.C.; Madison, L.L.; Kolter, R.; Walsh, C.T.
Science 274, 1188-1193, 1996
                                                                                                                                                                                                                                                          A;Cross references: GB:M24253; NID:g341145; PIDN:AAA72741.1; PID:g522290 R;Connell, N.; Han, Z.; Moreno, F.; Kolter, R. Mol. Microbiol. 1, 195-201, 1987 A;Title: An E. coli promoter induced by the cessation of growth. A;Reference number: I41099; MUID:88216163; PMID:2835580 A;Accession: I41099
A;Status: preliminary; translated from GB/EMBL/DDBJ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               A;Title: DNA sequence, products, and transcriptional pattern A;Reference number: A32058; MUID:89123111; PMID:2644225 A;Accession: A32058
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C;Species: Escherichia coli
C;Date: 30-Jun-1988 #sequence_revision 01-Dec-1995 #text_change 09-Jul-2004
C;Accession: A25219; A32058; I41099; A58368; S67977
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Nature 402, 761-768, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: H84489
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C;Date: 02-Feb-200
C;Accession: H8448
A;Title: From peptide precursors to oxazole and thiazole-containing peptide antibiotics A;Reference number: A58368; MUID:97053605; PMID:8895467
A;Accession: A58368
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A; Residues: 1-69 < GEN>
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A;Molecule type: DNA
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;Species: Arabidopsis thaliana (mouse-ear cress)
;Jate: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
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RESULT 5
E84686
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        R;Lin,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    hypothetical protein At2g28570 [imported] - Arabidopsis thaliana (Species: Arabidopsis thaliana (mouse-ear cress) C:Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004 C:Accession: E84686
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A,Title: Post-translational heterocyclic backbone modifications in
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A; Residues: 1-78 <STO>
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A; Residues: 27-38 <BAY>
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A,Note: mass spectroscopy of spectides and bloynthetic intermediates
R,Yorgey, P:, Lee, J.; Koerdel, J.; Vivas, E.; Warner, P.; Jebaratnam, D.; Kolter,
Proc. Natl. Acad. Sci. U.S.A. 91, 4519-4523, 1994
                                                                                                                                                                    A;Map
                                                                                                                                                                                                                                                   A;Cross-references: UNIPROT:Q9SK01; GB:AE002093; NID:g4510404; PIDN:AAD21491.1; GSPDB:GNO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           밁
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Molecule type: protein A; Residues: 27-38 <LIY>
                                                                                                                                                                                                                                                                                                                                     A;Status: preliminary
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Gene: At2g28570
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                                                                                                              Query Match
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Pred. No. 2
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Pred. No. 2.3e+02
                                                           Mismatches
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                                                                                    .6e+02;
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A;Cross-references: UNIPROT:Q04130; EMBL:X59883; NID:g19321; PIDN:CAA42538.1; PID:g19322 C;Superfamily: glycine-rich RNA-binding protein; ribonucleoprotein repeat homology
                                                                                                                                                                            R;Parsons, B.L. submitted to the EMBL Data Library, May 1991 A;Reference number: S19773
                                                                                                                                                                                                                                                               glycine-rich protein - tomato (fragment)
C;Species: Lycopersicon esculentum (tomato)
C;Date: 30-Jun-1992 #sequence_revision 30-Jun-1992 #text_change 09-Jul-2004
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A;Residues: 1-18;19-24;25-31;32-38;39-45;46-51;52-56;57-60;61-65;66-71;72-77;78-81
A;Cross-references: UNIPROT:07M1T8
C;Comment: This protein is the product of the Ha locus and thus be the major factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              grain-softness protein - wheat (fragments)
C;Species: Triticum aestivum (common wheat)
C;Date: 05-Aug-1994 #sequence_revision 05-Aug-1994 #text_change 09-Jul-2004
C;Accession: PC1047
R;Jolly, C.J.; Rahman, S.; Kortt, A.A.; Higgins, T.J.V.
Theor. Appl. Genet. 86, 589-597, 1993
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A;Residues: 1-80 <BEV>
A;Residues: 1-80 <BEV>
A;Cross-references: UNIPROT: Q9SUF7; EMBL: AL080252; GSPDB: GN00062; ATSP: T12G13.70
A;Experimental source: cultivar Columbia; BAC clone T12G13
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C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 16-Jul-1999 #sequence_revision 16-Jul-1999 #text_change 09-Jul-2004
C;Accession: T10550
                                                                                                                             A; Molecule type: mRNA
A; Residues: 1-82 < PAR>
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A; Accession: PC2047
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                                                                                                                                                                     A; Accession: S1977
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A; Accession: T10550
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                         Query Match
Best Local
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ilarity 100.0%;
Conservative 0
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Score 28; DB 2; Le
Pred. No. 2.7e+02;
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Pred. No. 2.6e+02;
); Mismatches 0;
                                            Length 82;
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C;Date: 29-Oct-1999 PROGRAMMER C;Accession: T32664
C;Accession: T32664
R;Davidson, S.; Wohldmann, P.; Bauer, C.; O'Neal, D.
R;Davidson, S.
R;Bevan, M.; Terryn, N.; Ardiles, W.; Buysshaert, C.; Dasseville, ewes, H.W.; Rudd, S.; Lemcke, K.; Mayer, K.F.X. submitted to the Protein Sequence Database, April 2000
                                                                                                                      hypothetical protein R15A17,120 - Arabidopsis thaliana (;Speckes: Arabidopsis thaliana (mouse-ear cress) C;Deckes: Arabidopsis thaliana (mouse-ear cress) C;Date: 20-Apr-2000 #sequence_revision 20-Apr-2000 #text_change 09-Jul-2004 C;Accession: T48330
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A;Cross-references: UNIPROT:Q7M1T7
A;Experimental source: seed
C;Keywords: seed
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A;Title: Characterisation of the wheat Mr 15000 grain-s
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 RESULT 9
T32664
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C;Species: Triticum aestivum (common wheat)
C;Date: 19-May-1994 #sequence_revision 19-May-1994 #text_change 09-Jul-2004
C;Accession: PQ0743
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PQ0743
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C;Species: Caenorhabditis elegans
C;Datc: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Accession: PQ0743
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A; Residues: 1-85 < DAV>
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Pred. No. 3e+02;
; Mismatches
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A;Releters T25332
A;Accession: T25332
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Status: preliminary;
A;Molecule type: DNA
A;Residues: 1-102 <WIL>
A;Residues: 1-102 <WIL>
A;Cross-references: UNIPROT:062385; EMBL:Z82056; PI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Accession: T48330
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-97 <BEV>
A;Cross-references: UNIPROT:Q9LYX6; EMBL:AL163002
A;Experimental source: cultivar Columbia; BAC clone F15A17
C;Genetics:
                                                                                                                                                                                                                                                                               hypothetical protein T26H5.4 - Caenorhabditis elegans C;Speciles: Caenorhabditis elegans C;Speciles: Caenorhabditis elegans C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004 C;Accession: T25332 R;Gardner, A. submitted to the EMBL Data Library, November 1996 A;Reference number: Z20017
                                                                                                                                                                                                                                                                                                                                                                                                                RESULT 13
T25332
                                                          A;Introns: 13/1; ye/1
C;Superfamily: hypothetical protein K01D12.8
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C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000
C;Accession: T49621
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A; Introns: 13/1; 96/1
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A; Residues: 1-100 <SCH>
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A; Accession: T49621
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A;Introns: 7/1
                                                                                                                                 A;Gene: CESP:T26H5.4
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Pred. No. 3.2e+02;
                   Score 28; DB 2;
Pred. No. 3.3e+02;
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A;Residues: 1-104 <ROU>
A;Residues: 1-104 <ROU>
A;Cross-references: UNIPROT:080985; EMBL:AC004747; NID:g3413696; PID:g3413702
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.;
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, I
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter,
Nature 402, 761-68, 1999
A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana.
A;Reference number: A84420; MUID:20083487; PMID:10617197
A;Accession: F84656
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          hypothetical protein At2g26120 [imported] - Arabidopsis thaliana
N;Alternate names: hypothetical protein T19L18.7
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 24-Mar-1999 #sequence_revision 24-Mar-1999 #text_change 09-Jul-2004
C;Accession: T02612; F84656
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; submitted to the EMBL Data Library, August 1998
A,Description: Arabidopsis thaliana chromosome II BAC T19L18 genomic sequence.
A,Reference number: Z14681
A;Accession: T02612
                                                                                                                                                                                   A;Molecule type: mRNA
A;Residues: 1-104 <LEE>
A;Cross-references: UNIPROT:Q25055; DDBJ:D13744; NID:g1088433; PIDN:BAA02889.1; PID:d100:
C;Comment: This protein is a Gly- and His-rich protein and a constitutive protein of larv
                                                                                                                                                                                                                                                                                          R;Lee, S.Y.; Moon, H.J.; Kurata, S.; Natori, S.; Lee, B.L. Biol. Pharm. Bull. 18, 1049-1052, 1995
A;Title: Purification and cDNA cloning of an antifungal protein A;Reference number: JC4190; MUID:96073722; PMID:8535393
A;Accession: JC4190
                                                                                                                                                                                                                                                                                                                                                                                                                                                     holotricin 3 precursor - Holotrichia diomphalia
N;Alternate names: antifungal protein
C;Species: Holotrichia diomphalia
C;Date: 04-Oct-1995 #sequence_revision 10-Nov-1995 #text_change 09-Jul-2004
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A;Map position: 2
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A; Residues: 1-104 <STO>
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                                                                                                                                                                ;Keywords: hemolymph
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Pred. No. 3.3e+02;
Mismatches 0;
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69 GGGGS 73

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Search completed: November 21, 2004, 13:43:26 Job time : 2.54745~secs

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Result
No.
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Maximum DB seq length: 2000000000
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Maximum Match 100%
Listing first 45 summaries
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  Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.
                                                                                                                                                                                                                                                     Score
 Query
Match
                                                                                                                                                                                                                                                                                                                       UniProt_02:*
1: uniprot_sprot:*
2: uniprot_trembl:*
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 GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
                                                                                                                                                                                                                                                     DB
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PPK5 PERAM
Q9R4Y9
Q8H647
Q82GM4
Q8N2Z2
Q7EZW2
BAD01701
                                     Q6YY44
BAD17456
Q75IX3
AAS07084
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Q84YS5
Q943L9
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AAR22556
Q7XMY7
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Q13832
Q13833
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Q9R582
Q9UC00
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                                                                     Q8LNH3
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                                                    O8w238 glycine max
O9r58 neisseria m
O9uc00 homo sapien
O4226 arabidopsis
O9f1i5 enterococcu
O9tww2 sarcophaga
O13832 homo sapien
O491d5 lactuca satian
O7sup7 oryza sativ
O7gsb6 glardia lam
O84ys5 oryza sativ
O98c82 rhizobium 1
O7s28 neurospora
O81nh3 oryza sativ
O998c82 rhizobium 1
O7s28 neurospora
O81nh3 oryza sativ
O80y44 oryza sativ
O80y44 oryza sativ
Q8h647 oryza sativ
Q82gm4 streptomyce
Q82gm4 omo sapien
Q7ezw2 oryza sativ
Bad01701 oryza sat
                                     Bad17456 oryza sat
Q75ix3 oryza sativ
Aas07084 oryza sat
                                                                                                                                                                                                                     Q6x2s9 homo sapien
Aap83315 homo sapi
P82617 periplaneta
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Q64450 mus musculu
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alcaligenes
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SEQUENCE FROM N.A.

Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. NCBI_TaxID=9606;

Homo sapiens (Human)

Name=TIM23;

EMBL; AY

AY258588; AAP83315.1;

5

SEQUENCE

10 AA; 893 MW; 2D7A7165B8787878 CRC64;

TISSUE-Skin;

MEDLINE-22890074; PubMed=14527731;

MEYER R.G., Meyer-Ficca M.L., Jacobson B.L., Jacobson M.K.;

Meyer R.G., Meyer-Ficca M.L., Jacobson B.L., Jacobson M.K.;

"Human poly(ADP-ribose) glycohydrolase (PARG) gene and the common promoter sequence it shares with inner mitochondrial membrane translocase 23 (TIM23).";

Gene 314:181-190(2003)."

28 100.0 62 2 BAD03150 28 100.0 63 2 Q94E89 28 100.0 63 2 Q8VB65 28 100.0 64 2 Q6K665 28 100.0 64 2 Q6K665 28 100.0 64 2 Q6ERC8 28 100.0 64 2 Q6ERC8 28 100.0 65 2 Q94J57 28 100.0 65 2 BAD17269 28 100.0 66 2 Q9XZQ8 28 100.0 66 2 Q9XZQ8 28 100.0 66 2 Q9XTQ4
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DAD03150 Q94289 Q8V865 Q5K665 Q91NS5 Q6ERC8 Q6ERC8 Q625J7 Q94J57 BAD17269 Q9XZQ8 Q9XZQ8 Q9XZQ8 Q9XXQ4 Q9XXQ4 Q9XXQ4

ALIGNMENTS

RESULT 1 Q6X2S9 ID Q6X2

Q6X2S9; PRELIMINARY; Q6X2S9; Q5X2S9; C5-JUL-2004 (TrEMBLrel. 27, L 05-JUL-2004 (TrEMBLrel. 27, L 05-JUL-2004 (TrEMBLrel. 27, L

PRT; Created)

10 AA

05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
Translocase of the inner mitochondrial membrane (Fragment).

RP SEQUENCE FROM N.A. RC TISSUE-Skin; RA Meyer R.G., Meyer-Ficca M.L., Jacobson E.L., Jacobson M.K.; RT "Human poly (ADP-ribose) glycohydrolase (PARG) gene and the common RT promoter sequence it shares with inner mitochondrial membrane	DT 02-MAR-2004 (TrEMBLrel. 27, Last annotation update) DE Translocase of the inner mitochondrial membrane (Fragment). GN TIM23. OS Homo sapiens (Human). OC Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; OC Mammalia; Eutheria; Primata; Catarrhini; Hominidae; Homo. OX [11] TaxID=9606;		Query Match 100.0%; Score 28; DB 2; Length Best Local Similarity 100.0%; Pred. No. 2.2e+02; Matches 5; Conservative 0; Mismatches 0; Inde Qy 1 GGGGS 5
son E.L., Jacobson M.K.; see (PARG) gene and the common ner mitochondrial membrane	notation update) lal membrane (Fragment). ata; Vertebrata; Euteleostomi; ini; Hominidae; Homo.	10 AA.	3 2; Length 10; 2e+02; 0; Indels 0;
		·	Gaps 0;

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RESULT 3
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Gene 314:181-190(2003).

EMBL; AY258588; AAP83315.1;

NON TER 10 10

SEQUENCE 10 AA; 893 MW;
                     Q9R4Y9;
01-MAY-2000
01-MAY-2000
01-JUN-2000
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P82617;
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16-OCT-2001 (Rel. 40, Last sequence update)
05-JUL-2004 (Rel. 44, Last annotation update)
Pyrokinin-5 (Pea-PK-5) (FXPRL-amide).
Periplaneta americana (American cockroach).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta;
Neoptera; Orthopteroidea; Dictyoptera; Blattaria; E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            -1-0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          -!- SIMILARITY: Belongs to the pyrokinin family InterPro; IPR001484; Pyrokinin. PROSITE; PS00539; PYROKININ; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        the
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    Aromatic
                                                                                                                Q9R4Y9
                                                                                                                                                                                                                                                                                                                                                                                                           Amidation; Direct protein sequencing; Neuropeptide; MOD_RES 17 17 Leucine amide. SEQUENCE 17 AA; 1653 MW; 8527162EA45BBA54 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDLINE=20189894; PubMed=10723010; Predel R., Eckert M.;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     e American cockroach.";
Comp. Neurol. 419:352-363(2000).
- FUNCTION; Mediates visceral muscle contractile
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to a lesser extent in retrocerebral complex.
MASS SPECTROMETRY: MW=1651.7; METHOD=MALDI; RANGE=1-17;
NOTE=Ref.1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          activity).
TISSUE SPECIFICITY: Mainly in abdominal
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dehydrogenase
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Pred. No.
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Pred. No. 3.7e+02;
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Blattoidea;
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01-MAR-2002 (TrEMBLrel. 20, Created)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last sequence update)
01-MAR-2002 (TrEMBLrel. 20, Last annotation update)
07-2 factor (Fragment).
Glycine max (Soybean).
Glycine max (Soybean).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids
eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae; Glycine.
NCBI TaxID=3847;
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01-NOV-1996 (TrEMBLrel. 01,

01-NOV-1996 (TrEMBLrel. 24,

01-JUN-2003 (TrEMBLrel. 24,

Uridine kinase (EC 2.7.1.48)
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MEDLINE=94245619; PubMed=8188594;

Govindaraj S., Eisenstein E., Jones L.H.,

Chistoserdov A.Y., Davidson V.L., Edwards
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Ropp P.A., Traut T.W.;
Submitted (MAY-1996) to the
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Mammalia; Eutheria;
NCBI_TaxID=10090;
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Alcaligenaceae; Alcaligene
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GO:0016301; F:kinase activity; IEA.
GO:0016740; F:transferase activity; IEA
GO:0004849; F:uridine kinase activity;
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ilarity 100.0%;
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AA; 1510 MW; 6EEEAEB9D89D2661 CRC64;
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SEQUENCE FROM N.A.
MEDLINE-95110623; PubMed=7829572;
Pierschbacher M.D., Polarek J.W., Craig W.S., T
Sipes N.J., Harper J.R.;
J. Cell. Biochem. 56:150-154(1994).
J. Cell. Biochem. 56:150-154(1994).
GO; GO:0009611; P:response to wounding; TAS.
GO; GO:0009611; P:response to wounding; TAS.
                                                                                                                                                                                                                  Eukaryota; Metazoa;
Mammalia; Eutheria;
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01-MAY-2000
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Bacteria; Proteobacteria;
Neisseriaceae; Neisseria.
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01-JUN-2003 (TrEMBLrel. 24, La
Transferrin-binding protein 2
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MEDLINE=21471140; PubMed=11587508;
O'Grady K., Goekjian V.H., Naim C.J., Nagao R.T., Key J.L
"The transcript abundance of GmGT-2, a new member of the
"The transcript abundance from soybean, is down-regulated
                                                                                                                                                                                           NCBI_TaxID=9606;
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i; Hominidae; Homo.
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Best Local 9
  Matches
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Q9F1I5;
01-MAR-2001
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Q42226;
01-NOV-1996
                                                                                    MBDLINE=20453452; PubMed=10998166;
De Boewer E.H., Clewell D.B., Fraser C.M.;
De Boewer E.H., Clewell D.B., Fraser C.M.;
"Enterococcus facealis conjugative plasmid pAM373: complete nucleotide sequence and genetic analyses of sex pheromone response.";
Mol. Microbiol. 37:1327-1341(2000).
EMBL; AR002565; AR40421.1; -.
Hypothetical protein; Plasmid.
SEQUENCE 31 AA; 3509 MW; 4E19CB94B3DB9421 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; Z;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 25, Last sequence update)
01-NOV-1996 (TrEMBLrel. 25, Last sequence update)
01-OCT-2003 (TrEMBLrel. 25, Last annotation update)
Seed maturation protein (Fragment).
Arabidopsis thallana (Mouse-ear cress).
Arabidopsis thallana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosids;
eurosids II, Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                  Plasmid pAM373.
Plasmid; Firmicutes;
                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAR-2001 (TrEMBLrel. 16,
01-MAR-2001 (TrEMBLrel. 16,
01-OCT-2003 (TrEMBLrel. 25,
Hypothetical protein EP0010.
                                                                                                                                                                                                                                                                                                                                                                                                             Hypothetical
Name=EP0010;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TISSUE=Dry seeds of A.thaliana ecotype columbia;
Raynal M., Grellet F., Laudie M., Meyer Y., Cooke R., De
Submitted (FEB-1994) to the EMBL/GenBank/DDBJ databases
                                                                                                                                                                                                                                                                       SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                               NCBI_TaxID=1351;
                                                                                                                                                                                                                                                                                                                                                                                   Enterococcus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted
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                     Local
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Similarity
5; Conser
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ilarity 100.0%;
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Pred. No. 5.
                       Pred.
                                          Score 28;
  Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                      faecalis).
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4.9e+02;
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                                            DB 2;
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5.5e+02;
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Best Local S
Matches 5
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Q13832;
Q1-NOV-1996
    EMBL; A71007
GO; GO:0004872;
                                           MEDLINE=96209920; PubMed=8655154; Braun A., Maier E., Kammerer S., N"A novel sequence polymorphism in bradykinin B2-receptor gene."; Hum. Genet. 97:688-689(1996).
EMBL; X91663; CAA62851.1; -.
                                                                                                                                                                                                                                                                                                                     01-NOV-1996 (TrEMBLrel. 01, Created)
01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2003 (TrEMBLrel. 24, Last annotation update)
B2 bradykinin receptor basal promoter, allele BP-58
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Inse
Neoptera; Endopterygota; Diptera; Brachycera;
Sarcophagidae; Sarcophaga.
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09TWW2:
01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence up
01-JUN-2003 (TrEMBLrel. 24, Last annotation
                                                                                                                                                                                                                                                    Eukaryota; Metazoa;
Mammalia; Eutheria;
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                                                                                                                                                                                                                                                                                                    Homo sapiens (Human)
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Ishikawa M., Kubo T., Natori S.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TISSUE=LARVAL HEMOLYMPH;
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                                                                                                                                                                                   SEQUENCE FROM N.A.
                                                                                                                                                                                                                               NCBI_TaxID=9606;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NCBI_TaxID=7386;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Antibiotic; Insect immunity.
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DEVELOPMENTAL STAGE: EXPRESSION IN THE LARVAE
DEVELOPMENTAL STAGE: EXPRESSION IN THE LARVAE
AFTER THE INJURY OF THE BODY WALL REACHING A
10 HOURS. THE MAXIMUM LASTS FOR AT LEAST 3 HC
INDUCTION: IN RESPONSE TO INJURY OF THE BODY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E.COLI AND S.SONNEI.
TISSUE SPECIFICITY: SYNTHESIZED
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GO:0006952; P:defense response; IEA.
GO:0006805; P:xenobiotic metabolism;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FUNCTION:
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5; Conserv
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                                                                                                                                                                                                                                                                                                                                                                                                                                             PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BACTERICIDAL ACTIVITY AGAINST GRAM-NEGATIVE BACTERIA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              23
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                       F:receptor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3928 MW;
                                                                                                                                                                                                                                                         Primates;
                                                                                                                                                                                                                                                                               Chordata;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         EXPRESSION IN THE LARVAE STARTS THE BODY WALL REACHING A MAXIMUM
                       activity; IEA.
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Pred. No. 7.7e+02;
; Mismatches 0;
                                                                                                                                                                                                                                                    Craniata; Vertebrata; Euteleostomi; Catarrhini; Hominidae; Homo.
                                                                                                                                                                                                                                                                                                                                                                                                                                               PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ) (Boettcherisca peregrina).
Hexapoda; Insecta; Pterygota;
                                                                                                                                      Mueller
                                                                                                                the
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                                                                                                              promoter
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                                                                                                                                        В.
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                                                                                                                   Roscher A.A.
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01-NOV-1996 (TrEMBLrel. 01, Ca
01-NOV-1996 (TrEMBLrel. 21, La
01-JUN-2003 (TrEMBLrel. 24, La
B2 bradykinin receptor basal p
Homo sapiens (Human)
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                                                                                         Kuang H., Nevo E., Michelmore R.W.;
Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.
EMBL; AY193418; ARAR2556.1; -.
GO; GO:0003735; F:structural constituent of ribosome; IE:
Ribosomal protein.
                                                                                                                                                                                                                                                                                                                                                                                              Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; asterids; campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 05-JUL-2004 (TrEMBLrel. 27, Created)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
60S acidic ribosomal protein P3 (Fragment).
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Hum. Genet. 97:688-689(1996).
EMBL; X91664; CAA62852.1; -.
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Braun A., Maier E., Kammerer S., Muell
"A novel sequence polymorphism in the
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Mammalia; Eutheria;
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Search completed: November 21, 2004, 13:42:21 Job time : 5.77372 secs
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STRAIN-CV. Calmar;

Kuang H., Nevo E., Michelmore R.W.;

Kuang H., Nevo E., Michelmore R.W.;

"Heterogeneous Rates of Evolution at the Major Cluster Disease
"Heterogeneous Rates of Evolution at the Major Cluster Disease
Resistance Genes in Lettuce due to Distinct Genetic Processes.";

Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.

EMBL; AY193418; AAR22556.1; -.

EMBL; AY193418; AAR22556.1; -.

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AAR22556;
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
60S acidic ribosomal protein P3 (Fragment).
Lactuca sativa (Garden lettuce).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magmoliophyta; eudicotyledons; core eudicots; asterids;
campanulids; Asterales; Asteraceae; Cichorioideae; Cichorieae;
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SUMMARIES

25	24	23	22	21	20	19	18	17	16	15	14	13	12	11	10	9	80	7	Q	IJ	4	u	2	۲	Result No.
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•			Adh22061 Synthetic	Histone	Aae37195 Linker pe	Aag77868 MHC class		Aae30928 Gly8-Glu2	Aae30929 Gly8-Glu2	Abr44505 Peptide 1	Abr56404 Peptide 1	Aaw56163 New DNA s	Aaw18563 Novel fus	Abu09677 INF-beta-	Aab00159 Seven rep	8 sCD4-S	4	Aag77867 MHC class	Aau05183 Pain-reli	Adq28273 Peptide 1	σ		5 Synthe	Aab00157 Seven rep	Description

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156	156	156	156	156	157	157	157	157.5	157.5	158	158	160.5	163	163	164	164	168	168	
79.6		79.6		79.6	80.1	80.1	80.1	80.4	80.4	80.6	80.6	81.9	83.2	83.2	83.7	83.7	85.7	85.7	
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Aam28596	Abb35090	Aam16105	Adj36245	Adj36257	Adj36241	Abr44503	Abr56402	Adf89517	Adf89524	Aag51723	Adp48740	Abu40120	Adp48742	Adn42013	Adf89525	Adf89519	Adc87061	Aab70188	•
Peptide #	Peptide #	Peptide #	Self-coal	Self-coal	Self-coal	Peptide 1	Peptide 1	H-antigen	H-antiger	Arabidops	Linker pe	Protein e	Phagmid p	Amino aci	H-antiger	H-antigen	Human GPC	Peptide d	

ALIGNMENTS

AAB00157 standard; peptide; 08-FEB-2001 AAB00157; (first entry) 35 B

Seven repeat linker used in sCD4-SCFv(17b) fusion protein.

Fusion protein; HIV; human immunodeficiency virus; antibody; Fv; AIDS; acquired immune deficiency syndrome; neutralisation; infection; gene therapy; CD4; gpl20; glycoprotein; resistance; vaccination; binding domain; single chain antibody; chimera; chimeric protein.

Synthetic.

WO200055207-A1

21-SEP-2000.

16-MAR-2000; 2000WO-US006946.

16-MAR-1999; (USSH) US NAT INST OF HEALTH 99US-0124681P.

Berger EA, Del Castillo CM;

WPI; 2000-638183/61.

Novel neutralizing bispecific fusion proteins effective in viral such as HIV neutralization, comprises two different binding domains, inducing-binding domain and induced-binding domain functionally linked by linker.

Claim 32; Page 45; 55pp; English.

RESULT 1
AABOO157
ID AABO
XX AABO
XX AABO
XX Seve
XX Seve
XX Fusi
KW Fusi
KW Gene
KW bind
XX WO20
XX Synt
XX Synt
XX WO20
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PR 16-W sCD4-SCFv(17b) is a neutralising bispecific fusion protein capable of binding to two sites of its target protein. The protein comprises a first binding domain capable of binding to an inducing site on the target protein, a second binding domain capable of forming neutralising complex with an induced epitope of the target protein and a linker connecting the binding domains. SCD4-SCFv(17b) comprises a soluble CD4 fragment (containing domains D1 and D2) fused to a single chain Fv portion of antibody 17b via a linker. SCD4-SCFv(17b), its variant, analogue or mimetic is used for inactivating gp120 protein of HIV, and for neutralising HIV. It is also used for blocking and preventing the binding of the viral or recombinant gp120 protein to soluble CD4 or lymphocyte

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   This invention relates to novel vector constructs for the expression of streptavidin fusion proteins. Streptavidin (SA) is produced by Streptowyces avidini and specifically binds water-soluble biotin. The vectors comprise a nucleic acid sequence encoding genomic streptavidin, promoter operatively linked to the nucleic acid sequence and a cloning site for insertion of a second nucleic acid sequence encoding an anti-CD25 antibody or its antigen binding fragment. The fusion proteins encoded are known as single chain antibody-genomic streptavidin fusion proteins (servSA). The vectors may have cytostatic activity when used ir gene therapy. The vectors may be useful in expressing genomic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  07-DEC-2001; 2001US-00013173.
17-MAY-2002; 2002US-00150762.
16-SEP-2002; 2002US-00244821.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                      New vector construct for expressing genomic streptavidin fusion proteins useful as diagnostic markers or as cell-specific targeting agents.
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CC protein and a protein capable of specifically binding to a cell surface contains of a reasonable region of an antibody, or it could comprise a ligand for a cellular receptor (e.g., a growth factor or a cytokine), the ligand combining domain of a cellular receptor, or the binding site of a cellular cellular receptor, or the binding site of a cellular cellular receptor, or the binding site of a cellular cellular receptor, or the binding site of a cellular cellular cellular cellular cellular cellular receptor, an integrin). The fusion protein additionally chas an amino acid substitution in the Fasi protein that decreases the ability of the Fasi portion of the fusion protein that decreases the cellular cel
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   New fusion protein useful for treatment of autoimmune disorders comprises a functional moiety of the extracellular domain of a Fas ligand protein and a polypeptide capable of specifically binding to a cell surface
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention relates to a fusion protein comprising the Fas protein recognition moiety of the extracellular domain of a Fas ligand (Fast
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Disclosure; Col 35-36; 26pp; English
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           04-APR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US6046310-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (PROT-) PROTEIN DESIGN LABS INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   invention
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 GGGGSGGGSGGGGSGGGGSGGGGS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Vasquez
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CHC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   96US-00614584.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               97US-00815190
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               and FasL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Queen CL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               domains
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 196; DB 6;
Pred. No. 6.6e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Mismatches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               protein.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0
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RESULT 4
AAB37196
ID AAB3
XX AAB3
XX AAB3
XX AAB3
XX Link
XX CD4-
XX CD4-
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XX HIV
XX WHIV
XX 24-A
XX 16-C
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XX 16-C
XX WPI
PH 16-C
XX WPI;
Y 10-C
XX The
CC PR 10-C
CC PR 10-
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Best Local S
Matches 35
     Best Loc
Matches
                                                         Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  target cells, and is less likely to cause apoptosis of non-target cells. The fusion proteins are useful for the treatment of various autoimmune disorders or other inflammatory conditions, including multiple sclerosis, rheumatoid arthritis, type I diabetes, inflammatory bowel disease, psoriasis, rejection of an organ transplant, or ischaemia- reperfusion injury, as well as for treatment of cancer. The present sequence represents an example of a linker which may be used to connect the CH3 domain of an immunoglobulin (Ig) to the FasL moiety in an Ig-FasL fusion
                                                                                                                                                                                     The invention relates to antibodies or antibody fragments specifically binding to CD4-inducible epitope on Human immunodeficiency virus (HIV) envelope glycoprotein (Env) proteins. The antibody is useful for preparing a composition for treating or preventing HIV infection. The invention is used to prepare vaccines and is used in gene therapy. The present sequence is a linker peptide used in the exemplification of the
                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                        Example 3; Page 67; 69pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New isolated antibody or antibody fragment specifically binds a CD4-inducible epitope on Human Immunodeficiency Virus (HIV) Env proteins, useful for preparing a composition for treating or preventing HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 2003-393518/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Dimitrov DS,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    16-OCT-2002; 2002WO-US033165.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-APR-2003
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CD4-inducible epitope; Human immunodeficiency virus; HIV; HIV infection; envelope glycoprotein; Env; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Linker peptide
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE37196 standard;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 40
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                                                                                                                                                                                                                                                                                                                                                                                                                                                     infection.
                            Local
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  l Similarity
35; Conserv
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US DEPT HEALTH & HUMAN SERVICES.
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                                                                                                                   40
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100.0%; Score 196; DB 6; ilarity 100.0%; Pred. No. 7.3e-12; Conservative 0; Mismatches 0:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ΑĄ;
                                                                                                             B
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moulard M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptide;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         glycoprotein; Env; vaccine.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Xiao
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Pred. No. 7.3e-12;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ×
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Phogat SK,
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                                                      Length 40;
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     Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Zhang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene therapy;
  ٥,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            0;
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  Gaps
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밁 S

24-OCT-2001 AAU05183; AAU05183

(first entry)

standard;

peptide;

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밁 S

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RESULT 6
AAU05183
ID AAU0
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AC AAU0
XX
DT 24-0
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ADQ28273
ID ADQ2
XX
AC ADQ2
XX
                                                                                                                                                                                                                           Query Match
Best Local S
Matches 35
                                                                                                                                                                                                                                                                                                                           The invention relates to a method of making a transgenic fusion protein comprising providing a transgenic animal which includes a transgene which provides for the expression of the fusion protein, allowing the transgene to be expressed, and recovering the fusion protein, from the milk of the transgenic animal. The methods and compositions of the present invention are useful for the diagnosis, prevention and/or treatment of colon, breast, prostate, ovarian and endometrial cancers. The present sequence represents the amino acid sequence of a peptide linker.
                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Making a transgenic fusion protein using a transgenic animal having a transgene expressing the fusion protein, useful for the diagnosing, preventing or treating colon, breast, prostate, ovarian and endometrial
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  gene therapy; tra
prostate cancer;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Edge MD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (EDGE/)
(POLL/)
(ECHE/)
(MEAD/)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-JUN-2003; 2003US-00608710.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADQ28273 standard; peptide; 40
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           18-SEP-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Peptide linker #1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             L7-SEP-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (RYBA/)
                                                                                                                                                                                                                                             Local Similarity
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                                                                                                                                                                                        μ
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DEDGE M D.
POLLOCK D.
ECHELARD Y.
MEADE H M.
RYBAK S M.
                                                                                                                                                                                        40 AA;
                                                                                                                                                        GGGGSGGGGGGGGGGGGGGGGGGGGGGGG
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pollock D,
                                                                                                                                                                                                                           100.0%;
ilarity 100.0%;
Conservative (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SEQ ID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      transgenic;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98US-0101083P.
99US-00398610.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ansgenic; fusion ovarian cancer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NO 6; 32pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Echelard Y,
                                                                                                                                                                                                                             0
                                                                                                                                                                                                                           Score 196; DB 8;
Pred. No. 7.3e-12;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ₿
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein; colon cancer;
endometrial cancer.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Meade HM,
                                                                                                                                                          36
                                                                                                                                                                                        35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     35
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Rybak SM
                                                                                                                                                                                                                                                             Length 40
                                                                                                                                                                                                                               Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        breast
                                                                                                                                                                                                                           0,
                                                                                                                                                                                                                           Gaps
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RESULT 7
AAG77867
ID AAG7
XX
AC AAG7
XX
AC AAG7
XX
DT 08-M
XX
XX
DT 08-M
XX
XX
MHC
XX
KW MHC
KW MHC
KW MHC
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                                                                                                                                                                                                                                       S
                                                                                                                                                                                                                                                                                                                              Query Match
Best Local S
Matches 35
                                                                                                                                                                                                                                                                                                                                                                                            The sequence represents the amino acid sequence of linker moiety #12 used to make a pain-relieving target construct. The construct comprises a pain relieving agent linked to a ligand moiety that selectively binds to or is taken up by the tissue associated with the painful interior disease site. The construct is used for treating pain associated with an interior disease este. Since the pain-relieving agent is delivered by the ligand to the disease site intractable pain situated in the interior of the body such as caused by various tumours, such as breast cancer, lung cancer, Hodgkin's and non-Hodgkin's lymphoma, and neuroblastoma, and ischaemic
MHC class II H domain spacer; IgG3-HLA fusion protein; major histocompatibility complex; MHC-peptide complex; MHC; MHC class II alpha chain; beta-2 microglobulin; MHC class II alpha chain;
                                                                                                                                                                                                                                                                                                                                                                  Hodgkin's and non-Hodgkin's lymphoma, and neuroblastoma, and ischaes and diseased tissues can be managed using a lower level of the pain relieving agent than is required when the pain-relieving agent is
                                                                                      08-MAY-2002
                                                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 21;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   administering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Treatment of pain associated with an interior disease site,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WPI; 2001-465198/50.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               08-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          06-DEC-2000; 2000WO-US042661.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      05-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Synthetic
                                                          MHC class II H
                                                                                                                                         AAG77867 standard; protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Luiken GA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (FLUO-) FLUORO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  WO200147512-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Misc-difference
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Hodgkin's
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Pain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pain-relieving target construct,
                                                                                                                                                                                                                                                                      35;
                                                                                                                                                                                                                                                                                     Similarity
                                                                                                                                                                                                                                   60
                                                                                                                                                                                                                                                                                                                                                        in the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 lymphoma; neuroblastoma;
                                                                                                                                                                                                                                                                                                                              Ā
                                                                                                                                                                                                                                                                   100.0%; llarity 100.0%; Conservative 0
                                                                                    (first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   a pain-relieving target construct
                                                       domain spacer
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PROBE INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               99US-00457498.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /note= "Each tetra-glycine repeat can optionally be glycine or tri-glycine" 8. .57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           88
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
3. .57
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /note= "Any amino acid'
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note= "Optionally absent"
                                                                                    entry)
                                                                                                                                                                                                                                                                                                                                                         state
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       31pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapeutic; breast cancer; lung cancer;
                                                                                                                                            60
                                                                                                                                                                                                                                                                      0
                                                                                                                                                                                                                                                                   Score 196; DB 4;
Pred. No. le-11;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linker moiety #12
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                                                                                                                                                                                                                                                                                               Length 60;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   involves
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MHC class II beta chain; vaccine; immune response modulation; hyperproliferative disorder; neoplasm; hypergammaglobulinaemia; viral infection; hepatitis; meningitis; bacterial infection; tuberculosis; gingivitis; parasitic infection; autoimmune disease; Hashimoto's disease; Graves' disease; rheumatoid arthritis; allergy; asthma; organ rejection; graft-versus-host disease; GVHD; HLA; human leukocyte antigen.

Synthetic.

WO200178768-A2.

25-OCT-2001.

12-APR-2000; 2001WO-US011912.

12-APR-2000; 2000US-0196472P.

(UYRP) UNIV ROCHESTER.

Zauderer M, Smith ES;
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Novel compound comprising major histocmpatibility complex-peptide complexes, used to modulate immune responses.

Example 3; Page 146; 166pp; English.

The present sequence represents a major histocompatibility complex (MHC) Class II H domain spacer. This protein was used as a replacement for the C class II molecules in an example of the invention CC detailing the construction of human IgG3-HLA fusion proteins. Absence of the H domain or a suitable spacer would result in misfolding of the MHC C class II molecule and the correct MHC binding site would not be formed. CC this invention comprises a compound which contains one or more major CC specific for a cell surface marker. The complexes, and an antibody CC specific for a cell surface marker. The complexes comprise an MHC class I specific for a cell surface marker. The complexes comprise an MHC class I class II alpha chain, a heft class II beta chain, and an antigenic peptide bound in the MHC groove. Alternatively, the complexes may comprise an MHC class II beta chain, and an antigenic compited bound in the MHC groove. The complexes are linked to the carboxyl terminus of the antibody. The compounds of the invention can be used as a creatine to modulate an immune response. The compounds of the invention can be used as a creatine to modulate an immune response. The compounds of the invention can be used as a creatine to modulate an immune response. The compounds of the invention compounds of the invention compounds of the invention and disparable infections; autoimmune diseases (e.g. hepatitis and meningitial); bacterial infections (e.g. hepatitis and gingivitis); conditions (e.g. asthma). The compounds of the invention may also be used in the treatment of organ rejection or graft-versus-host disease (GVHD)

Sequence 60 AA;

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RESULT 8
AAW18564
ID AAW1
XX
AC AAW1
AC AAW1
XX
DT 27-M
XX
DE Nove
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                                                                                                                                                   Best Loc
Matches
                                                                                                                                                                     Query Match
         Novel fusion protein KDTF7
                            27-MAR-1998
                                                                AAW18564 standard; protein; 312 AA
                                                                                                                                                   Local Similarity
les 35; Conserv
                                                                                                                                  GGGGSGGGSGGGSGGGSGGGSGGGS
                                                                                                                GGGGSGGGSGGGSGGGSGGGSGGGS
                            (first entry)
                                                                                                                                                   Conservative
                                                                                                                                                           100.0%;
                                                                                                                                                   0,
                                                                                                                                                  Score 196; D
Pred. No. 1e-
D; Mismatches
                                                                                                                                                    ະ 196;
ພາດ. 1e-11;
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                                                                                                                35
                                                                                                                                                   0
                                                                                                                                                                    Length 60
                                                                                                                                                    Indels
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                                                                                                                                                   Gaps
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RESULT 9
AABOO158
ID AABO
XX
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                                                                                                                                                                                                                                                                  CC This is a novel fusion protein comprising a factor VIIa (FVIIa) Kunitz CC type active site inhibitor domain sequence (AMN18553), a linker domain cC sequence, and a tissue factor (TF) domain sequence which is a human CC tissue factor variant hTFAA (AAW18556). This novel fusion protein has a Kunitz domain linked at its C-terminus via the peptide linker to the N-CC terminus of hFTAA. The novel fusion protein can be used for inhibiting thuman tissue factor-FVIIa (TF-FVIIa) procoagulant activity in a mammal. CC It can be used to treat TF-FVIIa related diseases like chronic CC including vascular disorders such as deep venous thrombosis, arterial CC thromboembolic diseases or disorders associated with fibrin formation CC including vascular disorders such as deep venous thrombosis, arterial CC treat acute and chronic disorders such as inflammation, septic Used to treat acute and chronic disorders such as inflammation, septic CC shock, adult respiratory distress syndrome, septicaemia, hypotension, CC disseminated intravascular coagulopathy and other diseases. Fusion CC sequence is not explicitly shown in the specification; it has been CC components alone or a non-covalent mixture of the two. Note: This sequence is not explicitly shown in the specification; it has been CC sequence given in Page 43 followed by a hTPAA sequence (AAW18553), a linker CC sequence given in Page 43 followed by a hTPAA sequence (AAW18556)
                                                                                                                                                                                        Query Match
Best Local
                                                                                                                                                                        Matches
                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Example 2; Page; 58pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Factor VIIa active site inhibitor domain and tissue factor fusion protein - used for inhibiting human tissue factor-FVIIa procoagulant activity in mammals, to treat e.g. thrombosis and restenosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-319785/29.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-DEC-1995;
04-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WO9720939-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  12-JUN-1997.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 thrombosis; human
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Kunitz type active site inhibitor domain; fusion protein; Factor VIIa; FVIIa; linker; tissue factor; TF; treatment; procoagulant activity;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (GETH ) GENENTECH INC.
                                                                                                       59
                                                                                                                                                                        l Similarity
35; Conser
                                                                                                                                                                                                                                             312
                                                                                                                              Lazarus RA,
                                                                                                                                                                                                                                           Ā
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              95US-00566459
95US-00566800
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "Kunitz type active site inhibitor domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /note= "tissue factor domain"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     note=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         . 93
                                                                                                                                                                                    100.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "linker peptide"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Lee
                                                                                                                                                                      0
                                                                                                                                                                      Score 196; DB 2;
Pred. No. 3.9e-11;
; Mismatches 0;
                                                                                                                                                                                                     Length 312;
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AAB00158 standard; protein; 507

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CC binding domain capable of binding to an inducing site on the target protein, a second binding domain capable of forming neutralising complex cc with an induced epitope of the target protein and a linker connecting the binding domains. sCD4-SCFV(17b) comprises a soluble CD4 fragment (containing domains D1 and D2) fused to a single chain FV portion of CC antibody 17b via a linker. sCD4-SCFV(17b), its variant, analogue or CC mimetic is used for inactivating pp120 protein of HIV, and for combinant gp120 protein of HIV, and for containing HIV. It is also used for blocking and preventing the binding CC of the viral or recombinant gp120 protein to soluble CD4 or lymphocyte CC data and for inhibiting HIV replication. The chimeric proteins is CC therefore useful for treating HIV infection and also AIDS. It is are particularly useful in the prevention of infection during or immediately after HIV exposure (e.g., mother/infant transmission, post-exposure CC prophylaxis, and as a topical linhibitor) and for providing long term CC resistance to HIV infections and AIDS. Gene therapy is used to secrete CC the bispecific protein at mucosal surfaces, such as the vaginal, rectal CC reactive with neutralising antibody with high in vivo activity and no Fc-mediated undesirable targetting properties. When the fusion protein is CC mediated undesirable targetting proteins, it has minimal immunogenicity and toxicity in humans which is of great value in prevention of infection CC during or immediately after HIV exposure
                                                                                                                                                  Matches
                                                                                                                                                                                                                                                                                            Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Novel neutralizing bispecific fusion proteins effective in viral such as HIV neutralization, comprises two different binding domains, inducing-binding domain and induced-binding domain functionally linked by linker.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              acquired immune deficiency syndrome; neutralisation; infection; gene therapy; CD4; gp120; g1ycoprotein; resistance; vaccination; binding domain; single chain antibody; chimera; chimeric protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     binding to two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               sCD4 -SCFv (17b)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 39; Page 46-47; 55pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Berger EA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   16-MAR-2000; 2000WO-US006946
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200055207-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fusion protein; HIV; human immunodeficiency virus; antibody; Fv; AIDS;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  sCD4-SCFv(17b) HIV single chain antibody fusion
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAB00158;
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                                                                                                                                          l Similarity
35; Conser
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAA54045
                                                                                                                                                                                                                                                                                                507
                                          Del Castillo CM
                                                                                                                                                  Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     is a neutralising bispecific fusion protein capable of sites of its target protein. The protein comprises a first
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             99US-0124681P
                                                                                                                                                                         100.0%;
                                                                                                                                          0,
                                                                                                                                          Score 196; DB 3;
Pred. No. 5.7e-11;
; Mismatches 0;
243
                                                                     35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      protein
                                                                                                                                                                                                           Length 507;
                                                                                                                                                  Indels
                                                                                                                                              0
                                                                                                                                          Gaps
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AAB00159 standard; peptide; 39

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CC binding to two sites of its target protein. The protein capable of the binding to two sites of its target protein. The protein comprises a first countries of the starget protein and a linker comprises a first countries. Scholars of binding to an inducing site on the target protein, a second binding domain capable of forming neutralising complex cut with an induced epitope of the target protein and a linker connecting the binding domains. Schol-ScFv(17b) comprises a soluble CD4 fragment (containing domains D1 and D2) fused to a single chain Fv portion of mimetic is used for inactivating gpl20 protein of HIV, and for neutralising HIV. It is also used for blocking and preventing the binding confidence of the viral or recombinant gpl20 protein to soluble CD4 or lymphocyte confidence useful for treating HIV infection and also AIDS. It is are particularly useful in the prevention of infection during or immediately capacitic protein at mucosal surfaces, such as the vaginal, rectal capacitic protein at mucosal surfaces, such as the vaginal, rectal creative with neutralising antibody with high in vivo activity and no Fc experience with neutralising antibody with high in vivo activity and no Fc expective with neutralising antibody with high in vivo activity and no Fc expected undesirable targetting properties. When the fusion protein is substantially derived from human proteins, it has minimal immunogenicity can convolve the full length CD4 coding sequence was excised from the plasmid pCB-3 using restriction enzymes Stul and Spel. Synthetic oligonucleotides (AAA54046) were ligated and used to regenerate the cleaved Stul site and the next two bases of the CD4 cONA and to produce an Spel (D14 and encodes the 37 amino acid intermediate linker as their described from the plasmid domain of CD4 and encodes the 37 amino acid intermediate linker as their described from its step shall site, forming pCD2. The 17b SCFv with the exact linker capacitic pmt tes step shall be a pCC3 and capacity and the capacitic pm its sequence was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Fusion protein; HIV; human immunodeficiency virus; antibody; Fv; acquired immune deficiency syndrome; neutralisation; infection; gene therapy; CD4; gp120; glycoprotein; resistance; vaccination; binding domain; single chain antibody; chimera; chimeric protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Novel neutralizing bispecific fusion proteins effective in viral such as HIV neutralization, comprises two different binding domains, inducing-binding domain and induced-binding domain functionally linked by linker.
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RESULT 11
ABRU99677
ID ABRU99
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Best Local S
                                                                                                                                                         molecule (I) or its variants, joined at one end to a first end of an immunoglobulin Fc fragment (II), without any linker between (I) and (II) or with a first linker between (I) and (II). The method is useful for treating tumours and viral infections including hepatitis B. The IFN-Fc hybrids have a much more longer half-life in vivo than the native IFNalpha. They are suitable for treating tumours such as lymphomas and leukaemias, as these products have the server treating tumours in time in the vasculature and will not penetrate undesired sites. The hybrids have been shown to ablate tumours in an animal model. At equivalent molar dosage of native IFN and the hybrid, the hybrid provides a several hundred fold
                                                                 efficacy at the same dosage and less frequent administration. This is the amino acid sequence of a linker that can be used to create an interferonbeta (INF-beta)-IgG4 fragment of crystallisation (Fc) fusion protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Interferon-beta; INF-beta; fragment of crystalisation; Fc; IgG4;
cytostatic; virucide; hepatotropic; antiinflammatory; tumour;
viral infection; interferon; INF; immunoglobulin Fc; hepatitis B;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The amplified fragment was digested with BamHI and SpeI and force-cloned into pCD2 to generate the sCD4-SCfv(17b) fusion protein in a plasmid designated pCD3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The invention describes a method of treating tumours or viral infections, involving administering a hybrid molecule having an interferon (IFN)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Treating tumors or viral infections, involves administering a hybrid molecule comprising an interferon molecule joined at one end to a fivend of an immunoglobulin Fc fragment, with or without a linker.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 2; Page 3; 9pp;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         15-OCT-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lymphoma; leukaemia;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (YULL/) YU L. (CHAN/) CHANG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Chang TW;
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97.1%;
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Pred.
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No. 1
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Best Local Similarity

89.8%;

Score Pred.

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Length

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Query Match

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      CC This is a novel fusion protein comprising a factor VIIa (FVIIa) Kunitz CC type active site inhibitor domain sequence (AAW18553), a linker domain CC tissue factor (TF) domain sequence which is a human CC tissue factor variant hTFAA (AAW18556). This novel fusion protein has a CC terminus of hFTAA. The novel fusion protein can be used for inhibiting CC human tissue factor FVIIa (TP-FVIIa) procoagulant activity in a mammal. CC It can be used to treat TF-FVIIa related diseases like chronic CC including vascular disorders such as deep venous thrombosis, arterial CC thromboembolic diseases or disorders such as deep venous thrombosis, arterial CC retenoses following angioplasty. The novel fusion protein can also be used to treat acute and chronic disorders such as inflammation, septic CC shock, adult respiratory distress syndrome, septicaemia, hypotension, CC proteins in which a FVIIa active site inhibitors and a tissue factor are CC covalently linked are more potent inhibitors of FVIIa than the individual components alone or a non-covalent mixture of the two. Note: This sequence is not explicitly shown in the specification; it has been linked.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Matches
                                                                                                                                                                                                                                                                                                                                              mammals, to treat e.g. thrombosis and restenosis.
                                                                                                                                                                                                                                                                                                                                                           Factor VIIa active site inhibitor domain and tissue factor fusion protein - used for inhibiting human tissue factor-FVIIa procoagulant activity in
                                                                                                                                                                                                                                                                                                                  Example
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Kelley RF, Lazarus RA,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-DEC-1995;
04-DEC-1995;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               22-NOV-1996;
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                                                                                                                                                                                                                                                                                                               2; Page; 58pp;
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95US-00566800.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             note= "Kunitz type active site inhibitor domain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                        Lee
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domain sequence TF71-C
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RESULT 14
ABR56404
ID ABR56
XX ABR56
XC ABR56
XC ABR56
XX 28-JU
XX 28-JU
XX Antig
KW cytog
KW cytog
KW antig
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AAW56163
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Best Local Similarity
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                                      Peptide linker #4.
                                                          28-JUL-2003
                                                                             ABR56404;
                                                                                               ABR56404 standard;
                                                                                                                                                                                                                          Sequence 738 AA;
                                                                                                                                                                                                                                               cosmetics
                                                                                                                                                                                                                                                      The present sequence represents protein encoded by isolated from Pinctada fucata. The protein be used
                                                                                                                                                                                                                                                                                  Claim 9; Page 9-11; 15pp; Japanese.
                                                                                                                                                                                                                                                                                                       New cDNA and e.g. vector, host cell and polypeptide - used to polypeptide in high yields, which is used in cosmetics.
                                                                                                                                                                                                                                                                                                                                     N-PSDB; AAV22683
                                                                                                                                                                                                                                                                                                                                               WPI; 1998-254410/23
                                                                                                                                                                                                                                                                                                                                                                                                                                               JP10080285-A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pinctada fucata
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Pinctada fucata;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       New DNA sequence isolated
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          28-JUL-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAW56163;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAW56163
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 307 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                sequence given in Page 43 followed by a hTFAA sequence (AAW18556)
                                                                                                                                                                                                                                                                                                                                                                                                        28-MAY-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                           31-MAR-1998
                                                                                                                                                                                                                                                                                                                                                                 (MIKI-) MIKIMOTO SEIYAKU KK.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Local Similarity
                                                                                                                                                666 GGGGSGGGSGGGSGGSGGSGGSGGSGGSGGGGS
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                                                         (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                      96JP-00184459
                                                                                                                                                                                                                                                                                                                                                                                                        97JP-00138461
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    protein; cosmetic
                                                                                              peptide;
                                                                                                                                                                                              88.0%;
78.6%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from Pinctada fucata.
                                                                                                41
                                                                                                                                                                                  Score 172.5;
Pred. No. 1.1e
0; Mismatches
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Pred. No. 3.3e-09;
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Antigen presenting cell; APC; immune response; virus like particle; VLP; cytostatic; virucide; antibacterial; antiparasitic; fungicide; antiallergic; immunosuppressive; antiaddictive; antiinflammatory;

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RESULT 15
ABR44505
ID ABR44
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AC ABR44
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AC ABR44
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25-JU
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                                                                                                                                                                                                                                                            Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A composition, useful for enhancing an immune response against an antigen or a virus-like particle, enhancing anti-viral protection in an animal, or immunizing or treating tumors or infectious diseases, e.g. viral
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Page 64;
    25-JUL-2003
                                                                                                                                                                                                                                                                                                                                          Sequence 41
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Bachmann MF,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         inflammatory autoimmune disease.
                                           ABR44505
                                                                               ABR44505 standard; peptide; 41 AA
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      (first entry)
                                                                                                                                                                                                                                                                              87.8%;
90.9%;
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                                                                                                                                                                                                                                                                              Score 172; DB 6;
Pred. No. 1.2e-09;
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Immunostimulatory; virus-like particle; bacteriophage; HBV; LCMV; hepatitis B virus; lymphocytic choriomeningitis virus; vaccine; immunostimulant; cytostatic; antiallergic; virucide; antibacterial; immune response; immunisation; allergy; tumour; breast cancer; neuroblastoma; leukaemia; viral disease; influenza; hepatitis; measles;
                                                                                                                                                                                                                                                   Pumpens
                                                                                                                                                                                                                                                                                                                   (MAUR/)
                                                                                                                                                                                                                                                                                                                                                14-SEP-2001; 2001US-0318994P.
22-APR-2002; 2002US-0374145P.
                                                                                                                                                                                                                                                                                                                                                                                                                             chicken pox; bacterial infection; tuberculosis; pneumonia; syphilis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Peptide linker
                                                                                                                                                                                                                                                                                                (MEIJ/)
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מְמָּאָ
                                                                                                                                                                                                                                                                         MEIJERINK E.
) LIPOWSKY G.
) PUMPENS P.
) CIELENS I.
) RENHOFA R.
                                                                                                                                                                                                                                                                                                             SCHWARZ K.
                                                                                                                                                                                                                                                                                                                      TISSOT A.
                                                                                                                                                                                                                                                                                                                            MAURER
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Cielens
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, Renhofa
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, Bachmann MF,
                                                                                                                                                                                                                                                      Lipowsky
, Storni
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WPI; 2003-354564/33.

New compositions comprising immunostimulatory substances packaged into virus-like particles, useful as a vaccine for enhancing an immune response in animals, e.g. for treating or preventing allergies, tumors or P

Disclosure; Page 75; 322pp; English.

The present invention describes a composition (C) for enhancing an immune response in an animal. (C) comprises a virus-like particle (VLP), and an climunostimulatory substance. The immunostimulatory substance is bound to the VLP, Also described: (1) enhancing an immune response in an animal by city introducing (C) into the animal; (2) producing (C) for enhancing an immune response in an animal by compare the response in an animal by administering comprising (C) together with a comparison of the animal by: (a) administering the vaccine to the animal; (b) priming a T cell response in the animal by administering the vaccine; or (C) boosting a T cell response in the animal by administering the vaccine; or (C) boosting a T cell response in the animal by administering the vaccine; or (C) thas immunostimulant, cytostatic, antiallergic, virucide and cantibacterial activities. (I) can be used in vaccines for enhancing an immune response, in an animal, particularly a mammal or human. (Specifically, (C) is useful for enhancing a B cell response, a T cell response, or a cytotoxic T-lymphocyte (CTL) response. (C) or a vaccine comprising (C) can also be used for immunising or treating an animal, ce.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds, ce.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds, ce.g. humans, sheep, horses, cattle, pigs, dogs, cats, rats, birds, comparison or succines against allergies, tumours (e.g. breast cancers, neuroblastoma, or leukaemial, varal diseases (e.g. influenza, hepatitis, meanimal or succines used in the exemplification of the present invention or succines used in the exemplification of the present invention

41 ₹

Query Match
Best Local Similarity
Matches 30; Conserv Conservative 87.8%; 0 Score 172; Pred. No. 1 Mismatches DB 6; 2e-09; Length 41 Indels 0 Gaps

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Result
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Match Length
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1: /ggn2_6/ptodata/1/iaa/5A_COMB.pep:*

2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*

3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*

4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*

5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*

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 GenCore version 5.1.6 (c) 1993 - 2004 Compugen Ltd.
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US-09-421-067C-4
US-09-421-067C-4
US-09-052-995-1
US-09-052-995-1
US-09-054-281-2
US-09-1818-094-40
US-09-1818-094-40
US-09-1818-094-40
US-09-1818-094-9
US-09-032-523-7
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3, Appli
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8, Appli
97, Appli
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RESULT 1		45	44	43	42	41	40	39	38	37	36	35	34	33	32	31	30	29	28
		138	138	138	138	138	138	138	138	138	138	138	139	140	140	140	٠	140.5	140.5
İ		70.4	70.4	70.4	70.4	70.4	70.4	70.4	70.4	70.4	70.4	70.4	70.9	71.4	71.4	71.4	71.7	71.7	71.7
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	ALIGNMENTS	US-08-469-318-194	PCT-US95-01185-50	US-09-510-238A-9	US-08-762-227A-50	US-08-446-872A-50	US-08-469-124-11	US-08-559-267A-11	US-08-192-325B-50	US-08-468-609A-50	US-08-469-318-50	US-08-470-775-11	US-09-543-681A-8322	US-09-538-092-990	US-09-543-681A-8319	US-09-254-832B-22	US-09-509-031-4	US-09-710-299-4	US-09-160-567-4
	•	Sequence 194, App	Sequence 50, Appl	Sequence 9, Appli		•	11,	11,	50,		50,	11,	Sequence 8322, Ap	Sequence 990, App	Sequence 8319, Ap	Sequence 22, Appl	Sequence 4, Appli	Sequence 4, Appli	Sequence 4, Appli

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US-08-815-190A-17
                                                                                                                                                  TELEPHONE: (415) 576-020
TELEPAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 40 amino acids
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 17, Application US/08815190A
Patent No. 6046310
                                                                                                                                                                                                                                                                                          ZIP: 94111-3834

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Vei

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/815,190A

FILING DATE: 11-MAR-1997

CLASSIFICATION DATA:

APPLICATION NUMBER: US 08/614,584

FILING DATE: 13-MAR-1996

ATTORNEY/AGENT INFORMATION:

NAME: APPLICATION NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 36,429

REFERENCE/DOCKET NUMBER: 011823-0067

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:

TELECOMMUNICATION INFORMATION:
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CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
CITY: San Francisco
STATE: California
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Queen, Cary L.
APPLICANT: Schneider, William P.
APPLICANT: Vasquez, Maximiliano
TITLE OF INVENTION: Fas Ligand Fusion Proteins and
TITLE OF INVENTION: Uses
                                                                                        MOLECULE TYPE:
FEATURE:
NAME/KEY: Peptide LOCATION: 6..40 OTHER INFORMATION: OTHER INFORMATION:
                                                                                                                                          TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          INFORMATION:
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                                                                                                                                                                                                                                                                            (415) 576-0300
                                                                                                                                        linear
/note= "amino acid residues 6-40 may be
present or absent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US/08/815,190A
                                                                                                                                                                                                                                                                                                                                                 011823-006710US
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Version
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APPLICANT: LUIKEN, George A.

APPLICANT: LUIKEN, George A.

TITLE OF INVENTION: METHOD FOR VIEWING TUMOR TISSUE LOC.

FILE REFERENCE: FLUORI120-2

CURRENT APPLICATION NUMBER: US/09/832,297A

CURRENT FILING DATE: 2001-04-09

PRIOR APPLICATION NUMBER: US 09/362,805

PRIOR FILING DATE: 1999-07-28

PRIOR APPLICATION NUMBER: US 09/173,190

PRIOR FILING DATE: 1998-10-15

NUMBER OF SEQ ID NOS: 12

SOFTWARE: Patentin version 3.1

SEQ ID NO 12

LENGTH: 60

TYPE: PRT

ORGANISM: Artificial sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/09333213
PATENT NO. 6548653
GENERAL INFORMATION:
APPLICANT: Young, Michael
APPLICANT: Meade, Harry
APPLICANT: Krane, Ian
TITLE OF INVENTION: ERYTHROPOIETIN ANALOGY-HUMAN SER
FILE REFERENCE: 10275/041001
CURRENT APPLICATION NUMBER: US/09/333,213
CURRENT APPLICATION NUMBER: US/09/333,213
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    RESULT 2
US-09-333-213-1
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SOFTWARE: FRATESEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 40
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 12, Application US/09832297A Patent No. 6652836 GENERAL INFORMATION:
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Best Local
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Best Local Similarity
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APPLICANT: LUIKEN, George
                                                        NAME/KEY: REPEAT LOCATION: (3)..(6) OTHER INFORMATION:
                                                                                                                                     OTHER INFORMATION:
                        NAME/KEY:
                                                                                                                     FEATURE:
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(3) .. (57)
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                                                          Amino
                                                                                                                                     Peptide linker moiety
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                                                          Acid
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                                                        3 could be repeated up
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GENERAL INFORMATION:

GENERAL INFORMATION:

APPLICANT: GE, LIMING

APPLICANT: GE, LIMING

APPLICANT: LIAG, VIC

APPLICANT: LIAG, VIC

APPLICANT: LIAG, VIC

FITTLE OF INVENTION: NOUTL METHOD AND PHAGE FOR THE IDENTIFICATION OF

TITLE OF INVENTION: NUCLEIC ACID SEQUENCES ENCODING MEMBERS OF A MULTIMERIC

TITLE OF INVENTION: (POLY) PEPTIDE COMPLEX

FILE REFERENCE: MORPHO/9

CURRENT APPLICATION NUMBER: US/09/495,880A

CURRENT APPLICATION NUMBER: US/09/495,880A

CURRENT APPLICATION NUMBER: POT/EP98/04836

PRIOR FILING DATE: 1998-08-03

PRIOR FILING DATE: 1998-08-03

PRIOR FILING DATE: 1998-08-03

PRIOR FILING DATE: 1997-08-01

NUMBER OP SEQ ID NOS: 50

SOFTWARE: Patentin Ver. 2.1

LENGTH: 465
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FILE REFERENCE: NUVASI140
CURRENT APPLICATION NUMBER: US/09/411,067C
CURRENT FILING DATE: 2002-05-07
NUMBER OF SEQ ID NOS: 5
SOFTWARE: Patentin version 3.0
SEQ ID NO 4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: NUVAS, LLC
APPLICANT: HOUSTON,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 4, Application Patent No. 6576610
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   TYPE: PRT
ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TYPE: PRT ORGANISM: Artificial sequence
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LOCATION: (1)..(5)
OTHER INFORMATION: Spacer peptide variation; sequence repeated "n" times, where n =
OTHER INFORMATION: 1-20
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OTHER INFORMATION:
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FEATURE:
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Local Similarity 100.0%;
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35; Conserv
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Pred. No. 7.7e-12;
Mismatches 0;
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Pred. No. 1.2e-11;
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; OTHER INFORMATION: HAG)-gene IIIss encoded by phage vector fhag1A (circular)
US-09-495-880A-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     RESULT 6
US-08-864-038A-3
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                                                                  Matches
                                                                                                Query Match
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                                                                                                                                                                                                                                                                                                                   TELEFAX: (212)953-7733
INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
LENGTH: 738
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/08/8
FILING DATE: May 28, 1997
PRIOR APPLICATION DATA:
APPLICATION NUMBER: JP 8-18
FILING DATE: 15-July-1996
ATTORNEY/AGENT INFORMATION:
NAME: C. Bruce Hamburg
REGISTRATION NUMBER: 22,389
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: Kunio
                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: protein ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: F-
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:
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ADDRESSEE: 812-5 Hirano
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TITLE OF INVENTION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM COmpatible
OPERATING SYSTEM: Microsoft Windows
SOFTWARE: Word Perfect 6.1
SOFTWARE: WORD PATA:
                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (212)986-2340
TELEFAX: (212)953-7733
DRMATION FOR SEQ ID NO: 3:
                                                                                                                                              NAME/KEY: peptide LOCATION: from 1 to 738 IDENTIFICATION METHOD: E
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MEDIUM TYPE:
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STATE: Mie-pre
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                                                                                  Local
                                                                                                                                                                                                                  CELL TYPE: mantle
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                               2 GGG-----SGGGGSGGGSGGGSGGGGSGGGGS
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                                                                                Similarity
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XGY: linear
Mie-prefecture
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WENTION: NOVEL POLYPEPTIDE GENE CDNA, VECTOR
VENTION: CONTAINING SAID CDNA, HOST CELLS TRANSFORMED WITH SAID
VENTION: VECTOR, POLYPEPTIDE PRODUCED THEREBY, METHOD OF PRODUCING
VENTION: SAID POLYPEPTIDE, DNA ENCODING SAID POLYPEPTIDE AND ANTIBODY
                                                                Conservative
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78.6%;
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                                                                                                                                                 (by experiment)
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                                                                              Score 172.5; DB 3; Pred. No. 7.1e-09;
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                                                                Mismatches
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                                                                                             Length 738;
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                                                               Indels
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US-09-053-003-40
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                                                                                                                                                                                                                                                       Patent No. 6207391
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                           Sequence 40, Application Patent No. 6207391
                                                                                                                                                                                                                                                                                                                                                                                                                                               Matches
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Patent No. 618395
                                                                                                                                                                                                                                                                                                                                                                                                                                                                Best
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match
                                                                                                                    APPLICANT: Wu, Pengguang
APPLICANT: MCKInney, Judi
TITLE OF INVENTION: High-Th
TITLE OF INVENTION: Modulat
NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and T
STREET: Two Embarcadero C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO:
SEQUENCE CHARACTERISTICS:
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Parent, Annette S.
REGISTRATION NUMBER: 42,0
REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER: IBM PC Compatible OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Patentin Release #1.0, CURRENT APPLICATION DATA:
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MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: (415) 576-0200
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICANT: Flores, Osvaldo A.
TITLE OF INVENTION: High Throughput In Vitro Screening Assay
TITLE OF INVENTION: for Transcription Modulators
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT:
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FILING DATE: 31-MAR-1998
CLASSIFICATION: 435
                                                           ZIP: 94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                                                              Local
                                                                     COUNTRY:
                                                                                                        CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY:
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Two Embarcadero Center, Eighth Floor
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High-Throughput Screening Assays for Modulators of STAT4 and STAT6 Activity
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82.4%;
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                                                                                                                    Townsend and Crew LLP
Center, Eighth Floor
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Pred. No. 6.4e-09;
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OPERATING SYSTEM:

PC-DOS/MS-DOS

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Patent No. 6444421
GENERAL INFORMATION:
APPLICANT: Chung, Jay H.
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Best Local Similarity
                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Ve:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/054,281
FILING DATE: 02-APR-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 201 amino acids
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NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
                                                                                               CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: US 60/080,234
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    CORRESPONDENCE ADDRESS:
ADDRESSEE: Townsend and Townsend and Crew LLP
STREET: Two Embarcadero Center, Eighth Floor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION:
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OTHER INFORMATION: /production / production / procession / procession / procession / preservation / p
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TELEPHONE: (415) 576-0200
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                              FILING DATE: 03-APR-1997 PRIOR APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LOCATION: 105..201
OTHER INFORMATION:
OTHER INFORMATION:
OTHER INFORMATION:
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APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY: USA
ZIP: 94111-3834
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               San Francisco : California
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82.4%;
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/note= "Gly at positions 105-201 may
present or absent"
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/note= "Gly at positions 1-97 may be
present or absent"
US 08/826,622
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Pred. No. 6.4e-09;
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FEATURE:
OTHER INFORMATION: Description of Artificial Sequence:flexible linker
NAME/KEY: MOD RES
LOCATION: (1]..(97)
OTHER INFORMATION: Gly at positions 1-97 may be present or absent
NAME/KEY: MOD RES
LOCATION: (105)..(201)
OTHER INFORMATION: Gly at positions 105-201 may be present or absent
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                                                                                                                                                                                                                                                                                            APPLICANT: Shan, Bei
APPLICANT: Okamoto, Arthur Y.
APPLICANT: Tularik Inc.
APPLICANT: Tularik Inc.
APPLICANT: Tularik Inc.

ITITLE OF INVENTION: FXR Receptor-Mediated Modulation of Cholesterol
TITLE OF INVENTION: Metabolism
FILE REFERENCE: 018781-001310US
CURRENT APPLICATION NUMBER: US/09/478,948
CURRENT APPLICATION NUMBER: US 60/115,249
PRIOR APPLICATION NUMBER: US 60/115,249
PRIOR APPLICATION NOWBER: US 60/115,249
RIOR FILING DATE: 1999-01-07
NUMBER OF SEQ ID NOS: 6
SOFTWARE: Patentin Ver. 2.1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 6, Application US/09478948 Patent No. 6465258 GENERAL INFORMATION:
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                                     Query Match
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TELEFAX: (415) 576-0300
INFORMATION FOR SEQ ID NO: 3
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                             LENGTH: 201
TYPE: PRT
                                                                                                                                                                                                                                            ORGANISM: Artificial Sequence
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NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear MOLECULE TYPE: peptide
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OTHER INFORMATION: OTHER INFORMATION: OTHER INFORMATION: 1
Local Similarity 82.
nes 28; Conservative
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OTHER INFORMATION:
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NAME: Smith, Timothy L. REGISTRATION NUMBER: 35, REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: Modified-site LOCATION: 105..201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: Modified-site
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           28;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      4: 201 amino acids
amino acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                   85.7%;
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/note= "Gly at positions 105-201 may
present or absent"
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/note= "Gly at positions 1-97 may be
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                   Score 168; DB 4;
Pred. No. 6.4e-09
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 168; DB 4;
Pred. No. 6.4e-09;
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   Mismatches
                                   DB 4;
                                     Length 201;
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                                                                    Matches
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                                                                                                  Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION FOR SEQ ID NO: 40: SEQUENCE CHARACTERISTICS:
                                                                                    Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/818,094
FILING DATE: 26-Mar-2001
CLASSIFICATION: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           McKinney, Judi
TITLE OF INVENTION: High-Throughput Screening Assays for
McGulators of STAT4 and STAT6 Activity
                                                                                                                                                                                                                                                                                                                                                                               TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: Smith, Timothy L.
REGISTRATION NUMBER: 35,367
REFERENCE/DOCKET NUMBER: 018781-000800US
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/09/053,003
FILING DATE: 31-MAR-1998
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NUMBER OF SEQUENCES: 64
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                FEATURE
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                                                                  28;
                                                                                Similarity
                              LOCATION: 1..97
OTHER INFORMATION: /product= "OTHER"
/note= "Gly at positions 1-97 may be
                                                                                                                                                                                   NAME/KEY: Modified-site
LOCATION: 105..201
OTHER INFORMATION: /product= "OT
/note= "Gly at positions 105-201
                                                                                                                                                                                                                                                                                                                                            NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                 STRANDEDNESS: <Unknown>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE: (415) 576-0200
TELEFAX: (415) 576-0300
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CITY: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                   ENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Townsend and Townsend and Crew LLP
                                                                  Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       94111-3834
                                                                                                                                                                                                                                                                                                                                                                                                                               H: 201 amino acids amino acid
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                                                                               85.7%;
                                                                                Score 168; DB 4;
Pred. No. 6.4e-09;
                                                                                                                                                                                     may be
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                                                                                               Length 201;
                                                                Indels
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RESULT 12

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RESULT 13
US-08-835-099A-9
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                                                                                                                          COMPUTER: IBM COMPACIDATE
COMPUTER: IBM COMPACIDATE
OPERATING SYSTEM: DOS
SOFTWARE: FASESEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/835,099A
FILING DATE: 04-APR-1997
CLASSIFICATION: 514
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 083649/1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 9, Approx. No. 5874277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: CuraPatSeqFormatter Version SEQ ID NO 844
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CURRENT APPLICATION NUMBER: US/09/538,092
CURRENT FILLING DATE: 2000-03-29
PRIOR APPLICATION NUMBER: 60/127,352
PRIOR FILING DATE: 1999-04-01
PRIOR PPLICATION NUMBER: 60/178,965
PRIOR APPLICATION NUMBER: 60/178,965
PRIOR FILING DATE: 2000-02-01
NUMBER OF SEQ ID NOS: 1387
                                 APPLICATION NUMBER: 083649/1996
FILING DATE: 05-APR-1996
APPLICATION NUMBER: 97105508.2
FILING DATE: 03-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: REGNICK, David S
REGISTRATION NUMBER: 34,235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Giot, Loic APPLICANT: Mansfield,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     FILE REFERENCE: 15966-542
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
NAME/KEY: misc_feature
LOCATION: (0)...(0)
OTHER INFORMATION: Polypeptide Accession Number P04264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TITLE OF INVENTION: Protein-Protein Complexes and Method of Using Same
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ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                   ZIP: 02109
COMPUTER READABLE FORM:
MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          APPLICANT: SHINTANI, Yasushi
APPLICANT: NISHI, Kaznori
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TITLE OF INVENTION:
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TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NUMBER OF SEQUENCES:
                    REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                COUNTRY: UZIP: 02109
                                                                                                                                                                                                                                                                                                                                                                                  STATE:
                                                                                                                                                                                                                                                                                                                                                                                                                    STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Local Similarity 82.4 es 28; Conservative
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IBM Compatible
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82.4%;
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                              34,235
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0; Mismatches
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Pred. No. 3
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US-09-157-349-9
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Query Match
Best Local Similarity 63.6
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Best Local (
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                                                                                                                                     INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 268 amino acid
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INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                     REGISTRATION NUMBER: 34,235
REFERENCE/DOCKET NUMBER: 47342
TELECOMMUNICATION INFORMATION:
TELEPHONE: 617-523-3400
                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ for Windows Version 2.0
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/157,349
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: SHINTANI, Yasushi
APPLICANT: KISHI, Kaznori
APPLICANT: KAWAMOTO, Tomohiro
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TOPOLOGY: linear MOLECULE TYPE: protein
                                                                                         TOPOLOGY: li
                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: 97105508.2
FILING DATE: 03-APR-1997
ATTORNEY/AGENT INFORMATION:
NAME: Resnick, David S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM: MEDIUM TYPE: Diskett
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 18
CORRESPONDENCE ADDRESS:
ADDRESSEE: DIKE, BRONSTEIN, ROBERTS & CUSMAN, LLP
STREET: 130 Water Street
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                PRIOR APPLICATION DATA:
APPLICATION NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TITLE OF INVENTION: NOVEL PR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 268 amino acid
TYPE: amino acid
STRANDEDNESS: single
                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          STATE: MA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             / Match 77.6%;
Local Similarity 63.6%;
les 28; Conservative
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                                                                                                                                                                                                                                                                                                                                                                     FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02109
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                                                                                                                       single
                          77.6%;
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             1;
             Score 152; DB 3; Length 268; Pred. No. 2.2e-07; 1; Mismatches 5; Indels
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             10;
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; TYPE: amino acid
; STRANDEDNESS:
; TOPOLOGY: linear
; MOLECULE TYPE: peptide
US-09-046-985-15
Search completed: November 21, 2004, 13:44:44 Job time : 5.53467 secs
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US-09-046-985-15
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Patent No. 612123
                                                                                                                                                                                                                             Best
                                                                                                                                                                                                                                           Query Match
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                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (781) 861-9540 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
APPLICANT: Ben-Sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                 ATTORNEY/AGENT INFORMATION:
NAME: Brook, David E.
REGISTRATION NUMBER: 22,592
REFERENCE/DOCKET NUMBER: CMCC-614
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDLUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/046,985
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NUMBER OF SEQUENCES:
                                                                                                                                                                                                         y Match 76.5%;
Local Similarity 40.2%;
hes 35; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   STREET: Two Militia [CITY: Lexington STATE: Massachusetts
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY: U
ZIP: 02173
                                                                                                                                                                                                                                                                                                                                                                                                                                    TELEPHONE:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
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                                                                                                                                                                                                                                                                                                                                                                   LENGTH:
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                                                                    87 AYRWRLSHRPKDLYSIVRRADRGGGGS
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                                                                                                                                        GGGGSGGGGSGGGSKDFTAYRWRLSHRPKDLYSIVRRADRGGGGSGGGGGGGGGGGKDFT 86
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                                                                                                                                                                                                                                                                                                                                                                   190 amino acids
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                                                                                                                                                                                                                                                                                                                                                                                                                                        (781) 861-6240
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NOVEL MULTIVALENT LIGANDS WHICH MODULATE
                                                                                                                                                                                                           0
                                                                                                                                                                                                         Score 150; DB 3;
Pred. No. 2.5e-07;
0; Mismatches 0
                                                                                                     GGGGS 35
                                                                    113
                                                                                                                                                                                                             0
                                                                                                                                                                                                                                          Length 190;
                                                                                                                                                                                                             Indels
                                                                                                                                                                          GGGGSGGGGS----
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Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries
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Maximum DB seq length: 200000000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Total number of hits satisfying chosen parameters:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Title:
Perfect score:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Run on:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         OM protein - protein search, using sw model
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BLOSUM62
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                November 21, 2004, 13:42:32; Search time 15.3285 Seconds (without alignments) 808.591 Million cell updates/sec
                                                                                 1570615 seqs, 354127592 residues
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            US-09-936-702-2
196
                                                                                                                                                                                                                                                                                                                                                                                     Published_Applications_AA:*

1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*

2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*

3: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*

5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
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          /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB_pep:*
/cgn2_6/ptodata/2/pubpaa/US08_REW_PUB_pep:*
/cgn2_6/ptodata/2/pubpaa/US08_REW_PUB_pep:*
/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
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/cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
/cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*
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Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

2 2 2 3 3 2 2 4 4 4 4 5 6 6 6 6 6 6 6 1 1 1 1 1 1 1 1 1 1 1 1	Result No.
196 196 196 196 196 196 196 196 196 196	Score
100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0 100.0	Query Match
25 25 25 35 35 35 35 35 35 35 35 35 35 35 35 35	Query Match Length DB
176 176 176 176 176 176	DB
US-10-013-173-30 US-10-150-762-30 US-10-244-821-30 US-10-281-400-1 US-10-257-864A-137 US-10-257-864A-138 US-10-608-710-6 US-10-768-873-1 US-09-949-039-32 US-09-833-297A-12 US-09-833-297A-12 US-09-833-203-18 US-10-437-963-126553 US-10-425-115-288960	ID
Sequence 30, Appl Sequence 30, Appl Sequence 30, Appl Sequence 1, Appli Sequence 137, Appli Sequence 138, Appli Sequence 6, Appli Sequence 1, Appli Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 12, Appl Sequence 126553, Sequence 288960,	Description

RESULT 2

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14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	14	10	10	10	10	9	9	9	10	17	15	15	17	15	17	
-10-123-	US-10-123-568-4		0-321-		-10-100-818-	US-10-293-582-27	0-245-	-10-233-	0-273-575-	-10-188-405-	US-10-094-417-25	-10-071-	-10-160-	-10-	0-026-021-	-10-160-	-09	-09-989-	US-09-990-940-21	US-09-921-159-34	US-09-998-667-18	09-967-624-1	84-	-09-833-	US-10-739-930-7816	-10-433-	-433-108-2	US-10-425-115-288955	-10-634-	-10-425-115-	
10	Sequence 4, Appli	12,	e 54,	18,		e 27	Sequence 3, Appli	ю 5,	29	e 13	e 25,	e 15,	ω '	س •	8	e 4,	e 29	13	e 21	e 34	18,		18,	e 19, Ap	e 781	e 25,	e 26	e 28	e 1	e 25	,

ALIGNMENTS

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APPLICANT: Lin, Yukang
APPLICANT: Sanderson, James A.
APPLICANT: Sanderson, James A.
APPLICANT: Sanderson, James A.
TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND TITLE OF INVENTION: METHODS OF USE THEREOF
FILE REFERENCE: 690022.547C1
CURRENT APPLICATION NUMBER: US/10/013,173
CURRENT APPLICATION NUMBER: US/10/013,173
CURRENT FILING DATE: 2001-12-07
NUMBER OF SEQ ID NOS: 69
SOFTWARE: FRANCESEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 35
TUDE: NOTE: 1000
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                                                                                                                                                            US-10-013-173-30
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                                                                            Query Match
Best Local S
Matches 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 30, Application US/10013173
Publication No. US20030095977A1
GENERAL INFORMATION:
APPLICANT: Goshorn, Stephen C.
APPLICANT: Graves, Scott Stoll
APPLICANT: Schultz, Joanne Elaine
                                                                                                                                                                           ORGANISM: Artificial Sequence FEATURE:
OTHER INFORMATION: Linker sequence
                                                                                                                                                                                                                                           TYPE: PRT
                                                                 Local Similarity 100.0%;
eB 35; Conservarion
                                 1 GGGGSGGGGSGGGGSGGGGSGGGGS
                                                                            0,
                                                                          Score 196; DB 14;
Pred. No. 2.6e-09;
D; Mismatches 0;
35
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                                                                                                                  Length 35;
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RESULT 4
US-10-081-400-1
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                                                                                                                                                                                                                        US-10-244-821-30
                                                                                                                                                                                                                                                                                                                            FILE REFERENCE: 690022.547C3
CURRENT APPLICATION NUMBER: US/10/244,821
CURRENT FILING DATE: 2002-09-16
NUMBER OF SEQ ID NOS: 92
SOPTWARE: FASTSEQ for Windows Version 4.0
SEQ ID NO 30
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NUMBER OF SEQ ID NOS: 90
SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 30
LENGTH: 35
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Publication No.
                                                                                                                                                Matches
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Best Local
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TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE
TITLE OF INVENTION: METAPLOS OF USE THEREOF
FILE REFERENCE: 690022.54702
CURRENT APPLICATION NUMBER: US/10/150,762
CURRENT FILING DATE: 2002-05-17
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Sanderson, James Allen
APPLICANT: Reno, John M.
APPLICANT: Dearstyne, Erica A.
TITLE OF INVENTION: STREPTAVIDIN EXPRESSED GENE FUSIONS AND
TITLE OF INVENTION: METHODS OF USE THEREOF
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICANT: Goshorn, Stephen Charles
APPLICANT: Graves, Scott Stoll
APPLICANT: Schultz, Joanne Elaine
APPLICANT: Lin, Yukang
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ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                                      LENGTH: 35
TYPE: PRT
ORGANISM: Artificial Sequence
FEATURE:
                                                                                                                                                                                                                                         OTHER INFORMATION: Linker sequence
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Lin, Yukang
Sanderson, James Allen
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10. US20030143233A1
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                                                                                                                                            100.0%; Score 196; DB 14; 100.0%; Pred. No. 2.6e-09; Mismatches 0;
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Pred. No. 2.6e-09;
; Mismatches 0;
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                                                                                                                                                                                  Length 35;
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APPLICANT: GOTEMBA-SHI, OHTOMO
TITLE OF INVENTION: AGONIST ANTIBODIES
FILE REFERENCE: 065678-0107
FILE REFERENCE: 065678-0107
CURRENT APPLICATION NUMBER: US/10/257,864A
CURRENT FILING DATE: 2003-07-24
PRIOR APPLICATION NUMBER: PCT/JP01/03288
PRIOR FILING DATE: 2001-04-17
PRIOR APPLICATION NUMBER: PCT/JP01/01912
PRIOR APPLICATION NUMBER: PCT/JP01/01912
PRIOR APPLICATION NUMBER: JP2000-115246
PRIOR FILING DATE: 2000-04-17
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: JP2000-321821
PRIOR APPLICATION NUMBER: JP2000-321822
PRIOR APPLICATION NUMBER: JP2000-321822
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
PRIOR FILING DATE: 2000-10-20
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APPLICANT: Krane, Ian
APPLICANT: Krane, Ian
TITLE OF INVENTION: ERYTHROPOIETIN ANALOGY-HUMAN SERUM ALBUMIN FUSION
TITLE OF INVENTION: ERYTHROPOIETIN ANALOGY-HUMAN SERUM ALBUMIN FUSION
CURRENT FILING DATE: 10275/041001
CURRENT FILING DATE: 2002-02-20
PRIOR APPLICATION NUMBER: US 09/333,213
PRIOR FILING DATE: 1999-06-15
NUMBER OF SEQ ID NOS: 4
SOFTWARE: FRStSEQ for Windows Version 4.0
SEQ ID NO 1
LENGTH: 40
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                                                                                                                                                                                                                                                                                                              NUMBER OF SEQ ID NOS: 138
SOFTWARE: PatentIn Ver. 2.1
SEQ ID NO 137
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 137, A Publication No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: FUKUSHIMA, NAOSHI
APPLICANT: TSUCHIYA, MASAYU
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Young, Michael
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           OTHER INFORMATION: Synthetically generated linker sequence; subsets 2 OTHER INFORMATION: consisting of a repetition of the first five amino OTHER INFORMATION: positions 6 through 40 may be absent or present
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: PRT ORGANISM: Artificial Sequence FEATURE:
FEATURE:
NAME/KEY: PEPTIDE
LOCATION: (1)..(40)
OTHER INFORMATION: This peptide may range from 1-40 amino acids;
OTHER INFORMATION: refer to the specification as filed for prefe
OTHER INFORMATION: embodiments
                                                                                                                                                                                                                                                              TYPE: PRT
                                                                                                                                                        OTHER INFORMATION: Description of Artificial Sequence: Synthetic OTHER INFORMATION: peptide
                                                                                                                                                                                                             FEATURE:
                                                                                                                                                                                                                                   ORGANISM: Artificial Sequence
                                                                                                                                                                                                                                                                                      LENGTH:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Local
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35; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 GGGGSGGGGSGGGGSGGGGSGGGGS
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OH-EDA, MASAYOSHI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    UNO, SHINSUKE
KIKUCHI, YASUI
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Pred. No. 2.9e-09;
; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PRIOR APPLICATION NUMBER: PCT/JP01/01912
PRIOR FILING DATE: 2001-03-12
PRIOR APPLICATION NUMBER: JP2000-115246
PRIOR FILING DATE: 2000-04-17
PRIOR APPLICATION NUMBER: JP2000-321821
PRIOR APPLICATION NUMBER: JP2000-321822
                                                Sequence 6, Application US/10608710
Publication No. US20040117863A1
GENERAL INFORMATION:
APPLICANT: GTC Biotherapeutics, Inc.
APPLICANT: Edge, Michael D
APPLICANT: Pollock, Daniel
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Best Local S
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Best Local Similarity
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OTHER INFORMATION: T
OTHER INFORMATION: r
OTHER INFORMATION: e
                   APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               APPLICANT: FUKUSHIMA, NAOSHI
APPLICANT: TSUCHIYA, MASAYUKI
APPLICANT: OH-EDA, MASAYOSHI
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NUMBER OF SEQ ID NOS: 138
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                  Echelard, Yann
Meade, Harry M
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ilarity 100.0%;
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Susanna M
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Pred. No. 2.9e-09;
; Mismatches 0;
                                                                                                                                                                                                                                                                                                              Score 196; DB 15;
Pred. No. 2.9e-09;
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RESULT 9
US-09-949-039-32
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                                                                                                                                                                                                               Sequence 32, Application US/09949039
Publication No. US20030166160A1
GENERAL INFORMATION:
SOFTWARE: PatentIn Ver.
SEQ ID NO 32
LENGTH: 50
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Best Local Similarity
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SOFTWARE: FastSEQ for Windows Version 4.0
SEQ ID NO 1
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Best Local Similarity
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                                                                TITLE OF INVENTION: COMPOUNDS AND MOLECULAR CY
TITLE OF INVENTION: BINDING REGIONS DIRECTED
FILE REFERENCE: 057220/1301
CURRENT APPLICATION NUMBER: US/09/949,039
CURRENT FILING DATE: 2001-09-06
NUMBER OF SEQ ID NOS: 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICANT: Meade, Harry
APPLICANT: Krane, Ian
ITILE OF INVENTION: ERYTHROPOIETIN ANALOGY-HUMAN SERUM ALBUMIN FUSION
PILE REFERENCE: 10275/041001
CURRENT APPLICATION NUMBER: US/10/768,873
CURRENT FILING DATE: 2004-01-30
PRIOR APPLICATION NUMBER: US/99/333,213
PRIOR APPLICATION NUMBER: US/99/333,213
PRIOR FILING DATE: 1999-06-15
                                                                                                                                                                                                 APPLICANT: HAWLEY, STEPHEN B.
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CURRENT FILING DATE: 2003-06-27
PRIOR APPLICATION NUMBER: US 09/398,610
PRIOR FILING DATE: 1999-09-17
NUMBER OF SEQ ID NOS: 11
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TYPE: PRT
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Pred. No. 2.9e-09;
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Pred. No. 2.9e-09;
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TITLE OF INVENTION: METHOD FOR VIEWING TUMOR TISSUE LOCATED WITHIN A BODY CAVITY FILE REFERENCE: FLUORIL20-2
CURRENT APPLICATION NUMBER: US/09/832,297A
CURRENT FILING DATE: 2001-04-09
FRIOR APPLICATION NUMBER: US 09/362,805
PRIOR PILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-07-28
PRIOR FILING DATE: 1999-10-15
NUMBER OF SEQ ID NOS: 12
SOFTWARE: Patentin version 3.1
SEQ ID NO 12
LENGTH: 60
TYPE: PAT
          Sequence 18, Application US/09833203

Publication No. US20030166277A1

GENERAL INFORMATION:
APPLICANT: Zauderer, Maurice
APPLICANT: Smith, Ernest S.
TITLE OF INVENTION: Targeted Vaccine Delivery Systems
FILE REFERENCE: 1821.0020001

CURRENT APPLICATION NUMBER: US/09/833,203

CURRENT FILING DATE: 2001-04-12

PRIOR APPLICATION NUMBER: US 60/196,472

PRIOR FILING DATE: 2000-04-12
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US-09-833-203-18
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                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: REPEAT
LOCATION: (3)..(57)
OTHER INFORMATION: Amino Acids at residues 3
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OTHER INFORMATION:
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SEQ ID NOS: 63
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Pred. No. 3.3e-09;
; Mismatches 0;
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Pred. No. 3.8e-09;
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APPLICANT: Zhou, Yihua

TITLE OF INVENTION: Nucleic Acid Molecules and TITLE OF INVENTION: Plants

FILE REFERENCE: 38-21(5322)B

CURRENT APPLICATION NUMBER: US/10/425,115

CURRENT TITLE OF APPLICATION NUMBER: US/10/425,115

CURRENT FILING DATE: 2003-04-28

NUMBER OF SEQ ID NOS: 369326

SEQ ID NO 288960

LENGTH: 250

TYPE: ppm
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ORGANISM: Artificial Sequence
NAME/KEY: misc_feature
OTHER INFORMATION: Spacer
US-09-833-203-18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           US-10-437-963-126553
; Sequence 126553, Application US/10437963
; Publication No. US20040123343A1
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US-10-425-115-288960
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       APPLICANT: Barbazuk, Brad
APPLICANT: Li, Ping
TITLE OF INVENTION: Rice Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants and Uses Thereof for Plant Improvement
FILE REFERENCE: 38-21 (53221) B
CURRENT APPLICATION NUMBER: US/10/437,963
CURRENT FILING DATE: 2003-05-14
NUMBER OF SEQ ID NOS: 204966
SEQ ID NO 126553
LENGTH: 211
TYPE: PRT
ORGANISM: Oryza sativa
FEATURE:
FEATUR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 288960, Application US/10425115 Publication No. US20040214272A1
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Best Local
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APPLICANT:
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APPLICANT: Kovalic, David
APPLICANT: Zhou, Yihua
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35; Conserv
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32; Conservative
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Pred. No. 1.1e-07;
0; Mismatches 2;
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Pred. No. 3.8e-09;
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RESULT 15
US-10-425-115-250884
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US-10-005-438-9
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US-10-005-438-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION NUMBER: 08/994,719
PRIOR FILING DATE: 1997-12-19
PRIOR APPLICATION NUMBER: 08/719,331
PRIOR FILING DATE: 1996-09-25
PRIOR APPLICATION NUMBER: 08/579,211
PRIOR FILING DATE: 1995-12-28
NUMBER OF SEQ ID NOS: 11
                                                              APPLICANT: LA ROSA, Thomas J.
APPLICANT: Kovalic, David K.
APPLICANT: Kovalic, David K.
APPLICANT: Cao, Yongwei
TITLE OF INVENTION: Nucleic Acid Molecules and Other Molecules Associated With
TITLE OF INVENTION: Plants
FILE REFERENCE: 38-21(53222)B
CURRENT FILING DATE: 2003-04-28
NUMBER OF SEQ ID NOS: 369326
SEQ ID NO 250884
                                                                                                                                                                                                                                                                               Sequence 250884, Application US/10425115
Publication No. US20040214272A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             GENERAL INFORMATION:
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PRIOR APPLICATION NUMBER: US/09/268,787
PRIOR FILING DATE: 1999-03-16
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APPLICANT: Liming Yu
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TYPE: PRT
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ORGANISM: Zea mays FEATURE:
                                  TYPE: PRT
                                                   ENGTH: 133
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Pred. No. 1e-07;
0; Mismatches 4;
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Pred. No. 1.9e-07;
0; Mismatches 0;
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Result
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Maximum Match 100%
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Perfect score:
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GenCore version (c) 1993 - 2004
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              RNA-binding protei
keratin, 59K type
glycine-rich prote
keratin, type II c
glycine-rich cell
glycine-rich RNA-b
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calpain (EC 3.4.22
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ALIGNMENTS

RESULT 1

glycine-rich protein Tfm5 - tomato (Species: Lycopersicon esculentum (tomato) (Species: Lycopersicon esculentum (tomato) (C;Date: 14-May-1999 #sequence_revision 14-May-1999 #text_change 09-Jul-2004 (C;Accession: T07381 R;Santino, C.G.; Stanford, G.L.; Conner, T.W. Plant Mol. Biol. 33, 405-416, 1997 PMID:9049262 A;Reference number: Z16000; MUID:97201476; PMID:9049262 A;Accession: T07381

fruit enhanced

genes

A;Modecule type: DNA A;Residues: 1-207 <SAN's A;Residues: 1-207 <SAN's A;Cross-references: UNIPROT:Q43522; EMBL:X95262; NID:g1166449; PIDN:CAA64559.1; PID:g116 A;Experimental source: cultivar UC82b; fruit

A;Status: preliminary; translated from GB/EMBL/DDBJ

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A;Reference number: Z15378
A;Accession: T04592
A;Molecule type: DNA
A;Residues: 1-221 <BEU's
A;Cross-references: UNIPROT:O65514; EMBL:AL022141
A;Experimental source: cultivar Columbia; BAC clone F23E13
                                                                                                                                                                                                                        C;Accession: T04592
C;Accession: T04592
R;Bevan, M.; Hilbert, H.; Braun, M.; Holzer, E.; Brandt,
á
              Query Match
Best Local Similarity
Marches 30; Conserv:
                                                                                                                                                                                                                                                                                  glycine-rich cell wall structural protein homolog F23E13.120 - Arabidopsis thaliana C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 23-Apr-1999 #sequence_revision 23-Apr-1999 #text_change 09-Jul-2004
                                                                                             A; Map position: 4
A; Note: F23E13.120
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C;Superfamily: hydroxyproline-rich glycoprotein
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 Similarity
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81.1%;
                                              82.7%;
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                             Score 162; DB 2; I
Pred. No. 5.3e-07;
0; Mismatches 5;
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                                                           Length 221;
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glycine-rich cell wall structural protein 1 precursor (clone lambda-313) - rice
C;Species: Oryza sativa (rice)
C;Date: 31-Dec-1991 #sequence_revision 31-Dec-1991 #text_change 09-Jul-2004
C;Accession: S13385
R;Lei, M.; Wu, R.
Plant Mol. Biol. 16, 187-198, 1991
A;Title: A novel glycine-rich cell wall protein gene in rice.
A;Reference number: S13385
A;Molecule type: DNA
A;Residues: 1-165 <LEI>
A;Cross-references: UNIPROT:P25074; EMBL:X53596; NID:g20246; PIDN:CAA37665.1; PID:g2
C;Genetics:
A;Gene: grp-1
C;Superfamily: glycine-rich cell wall structural protein 1
C;Keywords: cell wall; duplication; structural protein
F;1-23/Domain: signal sequence #status predicted <SIG>F;24-165/Product: glycine-rich cell wall structural protein
F;1-23/Domain: signal sequence #status predicted <SIG>F;62-92/Region: repeat R1
F;62-92/Region: repeat R2
F;100-131/Region: repeat R2
F;101-131/Region: repeat R1
F;132-138/Region: repeat R1
F;132-138/Region: repeat R1
F;132-138/Region: repeat R1
F;132-138/Region: repeat R1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      hypothetical protein C34D4.11 - Caenorhabditis elegans
C;Species: Caenorhabditis elegans
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T29282
R;Du, Z.; Le, T.T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 R;Du, Z.; Le, T.T.
submitted to the EMBL Data Library, May 1996
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Description: The sequence of A; Reference number: Z20600 A; Accession: T29282
                                                                                                                                                                                                                                                      A;Map position: 4
A;Introns: 20/1; 66/1; 98/1; 116/1
C;Superfamily: Arabidopsis glycine
                                                                                                                                                                                                                                                                                                                                                                                                              A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-136 <DUZ>
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RESULT 5
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A;Experimental source: strain Bristol N2; clone C34D4
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79.4%;
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Pred. No. 6.2e-07
1; Mismatches
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Pred. No. 6.6e-07;
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A;Residues: 1-592 cSIM>
A;Residues: 1-592 cSIM>
A;Cross-references: UNIPROT:OpPF60; GB:AE003921; GB:AE003849; NID:g9105710; PIDN:AAF83628; A;Cross-references: UNIPROT:OpPF60; GB:AE003921; GB:AE003849; NID:g9105710; PIDN:AAF83628; A;Sxperimental source: strain 9a5c
R;Simpson, A.J.G.; Reinach, F.C.; Arruda, P.; Abreu, F.A.; Acencio, M.; Alvarenga, R.; Al
Briones, M.R.S.; Bueno, M.R.P.; Camargo, A.A.; Camargo, L.E.A.; Carraro, D.M.; Carrer, H
as-Neto, E.; Docena, C.; El-Dorry, H.; Facincani, A.P.; Ferreira, A.J.S.
submitted to GenBank, June 2000
A;Authors: Ferreira, V.C.A.; Ferro, J.A.; Fraga, J.S.; Franca, S.C.; Franco, M.C.; Frohme
J.D.; Junqueira, M.L.; Kemper, E.L.; Kitajima, J.P.; Krieger, J.E.; Kuramae, E.E.; Laiger
Chado, M.A.; Madeira, A.M. B., Madeira, H.M.F.; Marino, C.L.; Marques, M.V.; Martins, E.
A;Authors: Martins, E.M.F.; Matsukuma, A.Y.; Menck, C.F.M.; Miracca, E.C.; Miyaki, C.Y.;
F.G.; Nunes, L.R.; Oliveira, M.A.; de Oliveira, M.C.; de Oliveira, R.C.; Palmieri, D.A
Rodrigues, V.; Rosa, A.J. de M.; de Rosa Jr., V.E.; de Sa, R.G.; Santelli, R.V.; Sawasaki
A;Authors: da Silva, A.C.R.; da Silva, F.R.; da Silva, A.M.; Silva Jr., W.A.; da Silva'
A;Reference number: A59328
                                                                                                                                                                                                                                                                                                                 A;Residues: 1-1226 <WIL>
A;Cross-references: UNIPROT:Q21835;
A;Experimental source: clone R08B4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Title: The genome sequence of the plant pathogen Xylella fastidiosa. A;Reference number: A82515; MUID:20365717; PMID:10910347 A;Note: for a complete list of authors see reference number A59328 bel A;Accession: E82759
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          endo-1,4-beta-glucanase XF0818 [imported] - Xylella fastidiosa (strain 9a5c)
C;Species: Xylella fastidiosa
C;Date: 18-Aug-2000 #sequence_revision 20-Aug-2000 #text_change 09-Jul-2004
C;Accession: E82759
R;anonymous, The Xylella fastidiosa Consortium of the Organization for Nucleotide Sequence 406, 151-157, 2000
밁
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A;Introns: 53/2; 113/1; 152/3; 204/3; 272/1; 354/1; 389/3; 714/3; 839/3; 877/1;
                                                                                                                                                                                                                                                                                                                                                                                                                       A; Status: preliminary; translated
                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Reference number: A; Accession: T24045
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               submitted to the EMBL Data A; Reference number: Z19834
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                R; White, S.
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hypothetical protein R08B4.1 -
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ;Species: Caenorhabditis elegans;Date: 15-Oct-1999 #sequence_revision
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71.8%;
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Pred. No. 4.1e-06;
1; Mismatches 5
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RESULT CIRBL

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calpain (EC 3.4.22.1
N;Alternate names: c
C;Species: Oryctolag
C;Date: 28-Dec-1987
A; Diacute Free: DNA A; Molecule type: DNA A; Molecule type: DNA A; Molecule type: DNA A; Residues: 144-146, 'P', 148-159, 'P', 161-183, 'K', 185-186 <CHI>A; Residues: 144-146, 'P', 148-159, 'P', 161-183, 'K', 185-186 <CHI>A; Cross-references: GB:M98776; GB:M11215; GB:M11845; GB:M11846; NID:g1843461 A; Cross-reference extracted from NCBI backbone (NCBIP:112784)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             C;Species: Homo sapiens (man)
C;Date: 04-Dec-1986 #sequence revision 22-Oct-1999 #text_change 10-Dec-1999
C;Accession: A22940; A02950; A43342
R;Johnson, L.D.; Idler, W.W.; Zhou, X.M.; Roop, D.R.; Steinert, P.M.
Proc. Natl. Acad. Sci. U.S.A. 82, 1896-1900, 1985
A;Reference number: A22940; MUID:85166239; PMID:2580302
A;Accession: A22940
                                                                                                                                                                                                                                                                                                       A;Cross-references: GB:M10938; NID:g186787; PIDN:AAA36153.1; PID:g386854
A;Experimental source: tissue neonatal foreskin
A;Note: the authors translated the codon CUG for residue 476 as Met
R;Chipev, C.C.; Korge, B.P.; Markova, N.; Bale, S.J.; DiGiovanna, J.J.; Compton, J.G.; (Cell 70, 821-828, 1992
A;Title: A leucine---proline mutation in the H1 subdomain of keratin 1 causes epidermol A;Reference number: A43342; MUID:92386601; PMID:1381288
A;Accession: A43342
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: DNA
A;Residues: 1-643 <JOH>
A;Note: translation of initiator Met is not shown
A;Note: translation of initiator Met is not shown
R;Steinert, P.M.; Parry, D.A.D.; Idler, W.W.; Johnson, L.D.; Steven, A.C.; Roop, D.R.
J. Biol. Chem. 260, 7142-7149, 1985
A;Title: Amino acid sequences of mouse and human epidermal type II keratins of M-r 67, A;Title: Amino acid sequences of mouse and human epidermal type II keratins of M-r 67, A;Title: Amino acid sequences of mouse and human epidermal type II keratins of M-r 67, A;Title: Amino acid sequences of mouse and human epidermal type II keratins of M-r 67, A;Title: Amino acid sequences of mouse and human epidermal type II keratins of M-r 67, A;Title: Amino acid sequences of mouse and human epidermal type II keratins of M-r 67, A;Title: Amino acid sequences of mouse and human epidermal type II keratins of M-r 67, A;Title: Amino acid sequences of mouse and human epidermal type II keratins of M-r 67, A;Title: Amino acid sequences of mouse and human epidermal type II keratins of M-r 67, A;Title: Amino acid sequences of mouse and human epidermal type II keratins of M-r 67, A;Title: Amino acid sequences of mouse and human epidermal type II keratins of M-r 67, A;Title: Amino acid sequences of mouse and human epidermal type II keratins of M-r 67, A;Title: Amino acid sequences of mouse and human epidermal type II keratins of M-r 67, A;Title: Amino acid sequences of mouse and human epidermal type II keratins of M-r 67, A;Title: Amino acid sequences of mouse and human epidermal type II keratins of M-r 67, A;Title: Amino acid sequences of mouse and human epidermal type II keratins of M-r 67, A;Title: Amino acid sequences of mouse and human epidermal type II keratins of M-r 67, A;Title: Amino acid sequences of mouse and human epidermal type II keratins of M-r 67, A;Title: Amino acid sequences of mouse and hu
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A;Note: Cleaves preferentially after tyrosine, methionine, or arginine
C;Superfamily: calpain small chain; calmodulin repeat homology
C;Keywords: calcium binding; cysteine proteinase; duplication; EF hand;
F;1-54/Domain: glycine-rich <GLY>
F;94-125/Domain: calmodulin repeat homology <EF1>
F;137-169/Domain: calmodulin repeat homology <EF2>
F;170-199/Domain: calmodulin repeat homology <EF3>
F;235-266/Domain: calmodulin repeat homology <EF3>
F;235-266/Domain: calmodulin repeat homology <EF5>
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R;Emori, Y.; Kawasaki, H.; Imajoh, S.; Kawashima,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         A;Molecule type: mRNA
A;Residues: 151-183,'K',185-199,'M',201-204,'K',206-236,'S',238-239,'R',241-356,'Y',358-
,'S',638-643 <STE>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A;Reference number: A92535; MUID:85207740; PMID:2581964
A;Accession: A02950
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    C; Function:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A; Cross-references: UNIPROT: P06813;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Molecule type: mRNA
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Alternate names: calcium-activated neutral proteinase (CANP); calpain light;
Species: Oryctolagus cuniculus (domestic rabbit);
Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004;
                                                                                                                                                                                                                                                              Status: preliminary; not compared with conceptual translation
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Pred. No. 2.6e-06;
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               are classified into two
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F;180-492/Domain: rod <ROD>
F;180-214/Region: coil 1A
F;215-226/Region: linker 1
F;227-327/Region: coil 1B
F;328-344/Region: linker 12
F;345-363/Region: linker 2
F;345-492/Region: linker 2
F;364-371/Region: linker 2
F;364-371/Region: coil 28
A;Cross-references: GDB:119752; OMIM:114170
A;Map position: 19pter-19pter
A;Introns: 70/2; 81/3; 111/3; 131/1; 152/3; 175/3; 202/1;
C;Complex: heterodimer of L (large) and S (small) chains C;Function:
                                                                                                                                                                                                                                                                   R;Ohno, S.; Emori, Y.; Suzuki, K.
Nucleic Acids Res. 14, 5559, 1986
A;Title: Nucleoride sequence of a cDNA coding for the small subunit
A;Reference number: A93631; MUID:86286563; PMID:3016651
                                                                                                                        A; Gene: GDB: CAPN4
                                                                                                                                               C; Genetics:
                                                                                                                                                                      A;Cross-references: EMBL:X04106; NID:g35327; PIDN:CAA27726.1;
                                                                                                                                                                                            A; Molecule type: mRNA
A; Residues: 1-268 < OHN>
                                                                                                                                                                                                                                               A; Accession: A23650
                                                                                                                                                                                                                                                                                                                                                                A;Cross-references: UNIPROT: P04632; GB:M31502
                                                                                                                                                                                                                                                                                                                                                                                         A; Molecule type: DNA
A; Residues: 1-268 < MIY>
                                                                                                                                                                                                                                                                                                                                                                                                                                       Nucleic Acids Res. 14, 8805-8817, 1986
A;Title: Gene organization of the small subunit of human calcium-activated neutral prote A;Reference number: A93648; MUID:87066759; PMID:3024120
A;Accession: A26107
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 C;Accession: A26107; A23650
R;Miyake, S.; Emori, Y.; Suzuki, K.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               C;Species: Homo sapiens (man)
C;Date: 28-Dec-1987 #sequence_revision 28-Dec-1987 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    calpain (EC 3.4.22.17) small chain - N; Alternate names: calcium-activated
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F;4-143/Region: E1 and V1 subdomains
F;14-179/Region: H1 subdomain
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   C;Superfamily: cytoskeletal keratin
C;Keywords: coiled coil; heterotetramer;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Note: defects in this gene may C; Complex: heterotetramer of two
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                A; Map position:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   A; Gene: GDB: KRT1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           atin IF protein subunit appears to be a heterotetramer of two type I and two type II C_1Comment: Keratin 1 is expressed in terminally differentiating epidermis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   F;513-643/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         F;493-512/Region:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  F;493-643/Domain:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Query Match
Best Local :
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Matches
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V2 and E2 subdomains
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82.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 153; DB 1;
Pred. No. 6.3e-06;
); Mismatches 6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      human
neutral proteinase
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                                                    241/1; 260/3
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                                                                                                                                                                        PID:g35328
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                                                                                                                                                                                                                                                                                               of human
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F;1-56/Domain: glycine-rich GLY>
F;96-127/Domain: calmodulin repeat homology <EF1>
F;139-171/Domain: calmodulin repeat homology <EF2>
F;172-201/Domain: calmodulin repeat homology <EF3>

A; Description: catalyzes the hydolysis of peptides A; Note: cleaves preferentially after timedulin repeat homology C; Superfamily: calpain small chain; calmodulin repeat homology C; Keywords: calcium binding; cysteine proteinase; duplication;

duplication; EF hand;

heterodimer;

hyd

or arginine residues and

befo

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A;Molecule type: DNA A;Residues: 1-255 <STO>A;Cross-references: UNIPROT:Q9SIH2;C;Genetics:
                                                                                                                                                                                                                                                                                                                                                                                 R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.B.; Umayam, L.; Tallon, Jeuss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; Vanaken, S.E.; Umayam, L.; Tallon, L. euss, D.; Nierman, M.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, Nature 402, 761-768, 1999
                                                                                                                                                                                                                                                                                                   A;Accession: F84797
A;Status: prelimina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             hypothetical protein At2g37830 [imported] - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            A;Map position: 2
C;Superfamily: collagen alpha 1(V) chain; fibrillar collagen carboxyl-terminal homology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana. A;Reference number: A84420; MUID:20083487; PMID:10617197 A;Accession: B84777
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F;237-268/Domain:
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                                   ફ
                                                                                                                                                                                                                        A;Cross-references: UNIPROT:Q7XJP7;
C;Genetics:
                                                                                                                                                                                                                                                           A; Molecule type: DNA
A; Residues: 1-106 <STO>
                                                                                                                                                                                                                                                                                                                                         A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487; PMID:10617197
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C;Species: Arabidopsis thaliana (mouse-ear cress)
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Best Local S
Matches 29
                                                                                                                                                       Superfamily: Arabidopsis glycine-rich protein
                                                                                                                                                                                                   Gene:
                                                                                                                                                                                                                                                                                                     Status: preliminary
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63.6%;
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76.5%;
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54.7%;
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Pred. No. 4.8e-06;
                                                                                              Score 150; DB 2;
Pred. No. 2.6e-06;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Score 152; DB 1;
Pred. No. 3.8e-06;
                                                                                                                                                                                                                                      GB:AE002093; NID:g4895201; PIDN:AAD32788.1;
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R;Bevan, M.; Wedler, H.; Wambutt, submitted to the Protein Sequence A;Reference number: Z25016
A;Accession: T49109
                                                                                     N;Alternate names: protein AT4g22020
c;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Jun-2000 #sequence_revision 02-Jun-2000 #text_change 09-Jul-2004
C;Accession: T49109
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Gene
A;Map
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            R;Lin, X.; Kaul, S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujii, C.Y.; N. M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon, L.: eass, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter, J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  hypothetical protein At2g05580 [imported] - Arabidopsis thaliana (FSpecies: Arabidopsis thaliana (mouse-ear cress) C;Species: Arabidopsis thaliana (mouse-ear cress) C;Date: 02-Feb-2001 #sequence_revision 02-Feb-2001 #text_change 09-Jul-2004 C;Accession: C84470
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A;Cross-references: UNIPROT:Q98937; EMBL:U47276; NID:g1546783; PIDN:AAB08467.1; PID:g1546C;Superfamily: fork head DNA-binding domain homology F;143-234/Domain: fork head DNA-binding domain homology <FHD>
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                                                                                                                                                                                                                                                                                                                                 S
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             A; Molecule type: DNA
A; Residues: 1-302 <STO>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Title: Sequence and analysis of chromosome 2 of the plant Arabidopsis thaliana A;Reference number: A84420; MUID:20083487; PMID:10617197
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                                                                                                                                                                             glycine-rich protein - Arabidopsis thaliana
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    A;Status: preliminary
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Nature 402, 761-768,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Gene: At2g05580
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;Date: 12-Feb-1998 #sequence_revision 13-Mar-1998 #text_change 16-Aug-2004
                                                                                                                                                                                                                                                                                                                                                                                  Matches
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49.1%;
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76.5%;
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Pred. No. 8.8e-06;
3; Mismatches 3
                                              R.; Bancroft, I.; Mewes, Database, May 2000
                                                                                                                                                                                                                                                                                                                                                                                                       Score 149; DB 2;
Pred. No. 7.2e-06;
                                                                                                                                                                                                                                                                                                                                                                                  Mismatches
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                                                                   Rudd,
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A; Molecule type: DNA A; Residues: 1-396 <B

1-396 <BEV>

A;Cross-references: UNIPROT:065450; EMBL:AL022140; GSPDB:GN00062; ATSP:AT4g22020

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A; Status: preliminary

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hypothetical protein T20B6.3 - Caenorhabditis elegans
(;Species: Caenorhabditis elegans
C;Date: 20.5ep-1999 #sequence_revision 20-Sep-1999 #text_change 09-Jul-2004
C;Accession: T15126
R;Beck, C.; Wamsley, P.
submitted to the EMBL Data Library, April 1997
A,Pescription: The sequence of C. elegans cosmid T20B6.
A;Reference number: Z18297
A;Recession: T15126
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Reference type: DNA
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A;Introns: 9/2; 231/1
C;Superfamily: Phaseolus glycine-rich protein 1.0
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C;Genetics:
A;Gene: ATSP:AT4g22020
A;Map position: 4
C;Superfamily: Phaseolus glycine-rich cell wall protein 1.8
Search completed: November 21, 2004, 13:43:27 Job time: 4.83212 secs
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A;Cross-references: UNIPROT:O02049; EMBL:AF000193; NID:g1946986; PID:g1946988; PIDN:AAB5
A;Experimental source: strain Bristol N2; Clone T20B6
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A; Gene: CESP: T20B6.3
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Best Local Similarity 53.7%;
Matches 29; Conservative
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Pred. No. 9.7e-06;
0; Mismatches 6; Indels 19; Gaps
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Post-processing: Minimum Match 0%
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Listing first 45 summaries
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196
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Q9GP44
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Q92nu8 oryza sativ
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Q8rus0 arabidopsis
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Q6s9v4 musca domes
Aar23812 musca domes
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Tfm5 protein.
Name=Tfm5;
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"Oryza sativa chromosome 3 BAC OSJNBa0024F18 genomic sequence."; submitted (OCT-2002) to the EMBL/GenBank/DDBJ databases.
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SEQUENCE
  Lycopersicon esculentum (Tomato).
Eukaryota; Viridiplantae; Streptophyta; Embryo
Spermatophyta; Magnoliophyta; eudicotyledons;
lamiids; Solanales; Solanaceae; Solanum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Submitted (JAN-2004) to the EMBL/GenBank/DDBJ databases EMBL; AC135594; AAR89849.1; -. SEQUENCE 551 AA; 59192 MW; 34C1EC87BB3CA297 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Oryza sativa (japonica cultivar-group).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza; Oryza sativa.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAR89849 PRELIMINARY; PRT; 551 AA.
AAR89849;
02-MAR-2004 (TrEMBLrel. 27, Created)
02-MAR-2004 (TrEMBLrel. 27, Last sequence update)
02-MAR-2004 (TrEMBLrel. 27, Last annotation update)
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OSJNBA0024F18.27.
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RESULT
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Best Local S
Query Match
Best Local Similarity
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PIR; T07381; T07381.
HSSP; P24337; 1HYP.
InterPro; IPR003612; AAI.
Pfam; PF00234; Tryp_alpha_amyl; 1
SMART; SM00499; AAI; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        01-AUG-1998 (TrEMBLrel. 07, Created)
01-AUG-1998 (TrEMBLrel. 07, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
05-JUL-2004 (TrEMBLrel. 27, Last sequence update)
Putative glyvine-rich cell wall protein.
Name=F23E13.120; Synonyms=AT4g36230;
Arabidopsis thaliana (Mouse-ear cress).
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; rosida
eurosids II, Brassicales; Brassicaceae; Arabidopsis.
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065514;
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                                                                                                                                           EU Arabidopsis sequencing project;
Submitted (MAR-2000) to the EMBL/GenBank/DDBJ
EMBL; AL02214; CAA18129.1; -
EMBL; AL161589; CAB80294.1; -
                                                                                                                                                                                                                                                                                            Hilbert H.,
Mewes H.W.,
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Hoheisel J., Jesse
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Bevan M., Hilbert H.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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Plant Mol.
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                                                                                  PIR; T04592; T04592.
InterPro; IPR002952; Eggshell.
PRINTS; PR01228; EGGSHELL.
                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                           Submitted (MAR-2000)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               207 AA;
                                                                                                                                                                                                                                                                                            Braun M., Holzer E., Brandt
Lemcke K., Mayer K.F.X.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Conservative
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                                                               AA;
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                                                                 20344 MW;
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  82.7%;
69.8%;
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  Score
Pred.
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Pred. No. 2.8e-06;
D; Mismatches 4
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L., Vos
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  162; DB 2;
No. 3.2e-06;
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Mewes H.W.,
                                                                                                                                                                                                                                                                                                                    Duesterhoeft
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                       Length
                                                                 CRC64;
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RESULT 7
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OS Rhiz
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Matches 27
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                   01-DEC-2001 (TrEMBLrel. 19, Created)
01-DEC-2001 (TrEMBLrel. 19, Last sequence update)
01-OCT-2002 (TrEMBLrel. 22, Last annotation update)
PUTATIVE GLYCINE-RICH PROTEIN.
OrderedLocusNames=R02073; ORFNames=SMC04357;
Rhizobium meliloti (Sinorhizobium meliloti)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        MEDLINE-21368234; PubMed-11474104; Galibert F., Finan T.M., Long S.R., Puehler A., Abola P., Ampe F., Barrloy-Hubler F., Barnett M.J., Becker A., Boistard P., Bothe G., Bartroy-Hubler F., Barnett M.J., Becker A., Cadleu E., Capela D., Chain P., Cowie A., Bowser L., Buhrmester J., Cadleu E., Capela D., Chain P., Goule A., Davis R.W., Dreano S., Federspiel N.A., Fisher R.F., Gloux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M., Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D. Kahn M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V., Wasuy D., Palm C., Peck M.C., Pohl T.M., Portetelle D., Purnelle B., Ramsperger U., Surzycki R., Thebault P., Vandenbol M., Vorhoelter F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J., Worhoelter F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J., William R., Cantal M., Wong K., Yeh K.-C., Batut J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J., Weidner S., Wells D.H., Weidner S., Weidner S
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SEQUENCE
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01-DEC-2002 (TrembLrel. 22, Last annotation update)
01-OCT-2002 (TrembLrel. 22, Last annotation update)
HYPOTHETICAL GLYCINE RICH TRANSMEMBRANE PROTEIN.
OrderedLocusNames=R01902; ORFNames=SMC04232;
Rhizobium mellloti (Sinorhizobium mellloti).
Bacteria; Proteobacteria; Alphaproteobacteria; Rhizobiales;
Rhizobiaceae; Sinorhizobium/Ensifer group; Sinorhizobium.
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                                                                                                                                                                                                                                   Q92NU7;
01-DEC-2001
                                                                                                                                                                                                                                                                                                              Q92NU7
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192 AA;
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                                                                                                                                                                                                                                                                                                              PRELIMINARY;
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18156 MW; 3B42C1F7F4322004
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79.4%;

    Created)
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Pred. No. 3.4e-06;
1; Mismatches 6;
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Best Local
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P25074;
01-MAY-1992 (Rel. 2
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                                                    This SWISS-PROT entry is copyright. It is produced through between the Swiss Institute of Bioinformatics and the Entropean Bioinformatics Institute. There are no restuse by non-profit institutions as long as its content
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Boutry M., Bowser L., Buhrmester J., Cadieu E., Capela D., Chain P., Cowie A., Davis R.W., Dreamo S., Federspiel N.A., Fisher R.F., Gloux S., Godrie T., Goffeau A., Golding B., Gouzy J., Gurjal M., Hernandez-Lucas I., Hong A., Huizar L., Hyman R.W., Jones T., Kahn D., Kahn M.L., Kalman S., Keating D.H., Kiss E., Komp C., Lelaure V., Masuy D., Palm C., Peck M.C., Pohl T.M., Portetelle D., Purnelle B., Ramsperger U., Surzycki R., Thebault P., Vandenbol M., Purnelle B., Ramsperger U., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J., Vorhoelter F.J., Weidner S., Wells D.H., Wong K., Yeh K.-C., Batut J., Science 293:668-672(2001).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spermatophyta; Magnoliophyta;
Ehrhartoideae; Oryzeae; Oryza
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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Plant WOTION: Responsible for plasticity of the Color SUBCELLULAR LOCATION: Cell wall (Potential).
                                                                                                                                                                                                                                                            Plant
                                                                                                                                                                                                                                                                                                                                           MEDLINE=91370862;
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                                                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                                                                                              Lei M., Wu
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PubMed=1716496;
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22, Last sequence update)
44, Last annotation update)
wall structural protein 1 precursor.
license agreement (See http://www.isb-sib.ch/announce,
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S., Gloux
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Matches 30
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                                                                                                                                                                   "Direct Submission.";
Submitted (SEP-2001) to the EN SMBL; US975; AAB00696.1; -. PIR; T29282; T29282
WormPep; C34D4.11; CE17505.
Hypothetical protein.
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Q18444;
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Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
Rhabditidae; Peloderinae; Caenorhabditis.
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Cell wall; Repeat; Signal;
SIGNAL 1 23
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Submitted (MAY-1996) to the EMBL/GenBank/DDBJ databases.
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STRAIN-Bristol N2;
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MEDLINE=99069613; PubMed=9851916;
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                                                                                                                                                     SEQUENCE
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                                                                                                                                                                                                                                                                                                         STRAIN-Bristol N2;
                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                "Genome sequence of the nematode C. elegans: a platform for investigating biology. The C. elegans Sequencing Consortium Science 282:2012-2018(1998).
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                                                                     Score 159; DB 2;
Pred. No. 3.7e-06;
1; Mismatches 6
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QBRUSO;
Q1-JUN-2002 (TrEMBLrel. 21, Last sequence update)
01-JUN-2002 (TrEMBLrel. 27, Last annotation update)
05-JUL-2004 (TrEMBLrel. 27, Last annotation update)
                                                        STRAIN-EBY-1;
STRAIN-EBY-1;
Delaroque N., Bothe G., Pohl T., Knippers R.,
Delaroque N., Bothe G., Pohl T., Knippers R.,
Submitted (MAR-2001) to the EMBL/GenBank/DDBJ
EMBL; AF204951; AAF28325.1; -.
EMBL; AF204951; AAF28325.1; -.
SEQUENCE 698 AA; 74035 MW; C7638DDB922E0Df
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Town C.D., Kaul S.;

Town C.D., Kaul S.;

Submitted (FEB-2002) to the EMBL/GenBank/DDBJ da

EMBL; AC006201; AAM15144.1; -.

EMBL; AC007212; AAM15455.1; -.

InterPro; IPR002952; Eggshell.

PRINTS; PR01228; EGGSHELL.

Hypothetical protein.

SEQUENCE 296 AA; 28644 MW; 8BD3FF446EA1E23F
                                                                                                                                                                                                                                                                                                                                           QBQXXXB;
                                                                                                                                                MEDLINE=20192171; PubMed=10725207; Delaroque N., Wolf S., Muller D.G., Knipp "Characterization and immunolocalization in the brown algal virus EBV-1."; Virology 269:148-155(2000).
                                                                                                                                                                                                                                             NCBI_TaxID=37665;
                                                                                                                                                                                                                                                         Ectocarpus siliculosus virus.
Viruses; dsDNA viruses, no RNA
                                                                                                                                                                                                                                                                                                                    01-JUN-2002
01-JUN-2002
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Barnstead M.E., Mason T.M., Bowman C.L., Ronning C.M., Ben
Carrera A.J., Creasy T.H., Buell C.R., Town C.D., Nierman
Fraser C.M., Venter J.C.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Arabidopšis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyla;edons; core eudicots; rosid
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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                                                                                                                            SEQUENCE FROM N.A.
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                      Score 157; DB Pred. No. 2.1e 1; Mismatches
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                                                                                          Mueller D.G., databases.
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AAR23812;
02-MAR-2004
02-MAR-2004
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Q6S9V4;
05-JUL-2004
05-JUL-2004
                                                                                                                                                                                    Hediger M., Burghardt G., Siegenthaler C., Buser N.,
Hilfiker-Kleiner D., Dubendorfer A., Bopp D.;
"Sex determination in Drosophila melanogaster and Musca domestica
converges at the level of the terminal regulator doublesex.";
Dev. Genes Evol. 214:29-42 (2004).
EMBL; AY461853; AAR23812.1;
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SEQUENCE 397 AA; 41701 MW; 38B49CED6931F8C4 CRC64;
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Hilfiker-Kleiner D., Dubendorfer A., Bopp D.;
"Sex determination in Drosophila melanogaster and Musca domestica
converges at the level of the terminal regulator doublesex.";
Dev. Genes Evol. 214:29-42(2004).
EMBL; AY461853; AAR23812.1; -.
InterPro; IPR001275; DM_DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Musca domestica (House fly).
Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Muscoidea;
Muscidae; Musca.
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PROSITE; PS50809; DM DOMAIN 2; 1.
SEQUENCE 397 AA; 41701 MW; 38
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Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Bueoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Muscoidea;
                                                                                                                                                                                                                                                                                                                                                                                              PubMed=14673649;
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SMART; SM00301; DM; 1.
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                                                           Score 156; DB Pred. No. 1.6e 2; Mismatches
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Eukaryota; Metazoa; Arthropo
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DSX.

Musca domestica (House fly).

Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;

Eukaryota; Muscomorpha; Muscoidea;
                                                                                  Heddiger M., Burghardt G., Siegenthaler C., Buser N., Hilfiker-Kleiner D., Dubendorfer A., Bopp D.; Hilfiker-Kleiner D., Dubendorfer A., Bopp D.; "Sex determination in Drosophila melanogaster and Musca domes converges at the level of the terminal regulator doublesex."; Dev. Genes Evol. 214:29-42(2004).

EMBL; AY461854; ARAC28813.1; -.

EMBL; AY461854; ARAC28813.1; -.

SEQUENCE 527 AA; 55663 MW; A71E04E000A6D421 CRC64;
                                                                                                                                                                                                                                                                                             Neoptera; Endopterygota; Diptera; muscidae; Musca. NCBI TaxID=7370;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             converges at the level of the terminal Dev. Genes Evol. 214:29-42(2004). EMBL; AY461854; AAR23813.1; -. InterPro; IPR001275; DM_DNA-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Hilfiker-Kleiner D., Dubendorfer A., Bopp D.; 
"Sex determination in Drosophila melanogaster and Musca domestica
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PS50809; DM_DOMAIN_2; 1.
527 AA; 55663 MW; A7
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Search completed: November 21, 2004, 13:42:23 Job time : 21.4161 secs

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SUMMARIES

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42 Chimeric	Aaw83142	AAW83142	N	462	39.7	1059	45
14 CD4:Fc re	Aaw02214	AAW02214	N	462	39.7	1059	44
57 CD4:gamma	Aar89457	AAR89457	N	462	39.7	1059	43
77 T-cell re	Aar78677	AAR78677	N	462	39.7	1059	42
_	Aar27277	AAR27277	N	462	39.7	1059	41
69 DNA encod	Aab07769	AAB07769	w	458	39.7	1059	40
26 Soluble h	Aay39826	AAY39826	ຎ	458	39.7	1059	39
•	Aar13491	AAR13491	N	458	39.7	1059	38
	Aap91369	AAP91369	ب	458	39.7	1059	37
_	Aap81990	AAP81990	ب	458	39.7	1059	36
-	Aap94757	AAP94757	ب	402	39.7	1059	35
	Aap91922	AAP91922	ب	402	39.7	1059	34
74 Truncated	Aar06374	AAR06374	N	400	39.7	1059	33
50 CD4 D1-D4	Aar89450	AAR89450	N	398	39.7	1059	32
~	Aar78673	AAR78673	N	398	39.7	1059	31
	Ade65841	ADE65841	7	458	39.8	1062	30
68 CD4-Ig f	Aay59168	AAY59168	ω	729		1064	29
78 Human fus	Aay51078	AAY51078	ú	729		1064	28
07 CD4-IgG1	Aab19507	AAB19507	w	729	39.9	1064	27
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AAB00158 standard; protein; 507

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ALIGNMENTS

AAB00158;

08-FEB-2001 (first entry)

sCD4-SCFv(17b) HIV single chain antibody fusion protein.

Fusion protein; HIV; human immunodeficiency virus; antibody; Fv; AIDS; acquired immune deficiency syndrome; neutralisation; infection; gene therapy; CD4; gpl20; glycoprotein; resistance; vaccination; binding domain; single chain antibody; chimera; chimeric protein.

Human immunodeficiency virus. Synthetic.

WO200055207-A1

21-SEP-2000

16-MAR-2000; 2000WO-US006946

16-MAR-1999; 99US-0124681P.

(USSH) US NAT INST OF HEALTH

Berger EA, Del Castillo CM;

N-PSDB; AAA54045. 2000-638183/61.

Novel neutralizing bispecific fusion proteins effective in viral such as HIV neutralization, comprises two different binding domains, inducing-binding domain and induced-binding domain functionally linked by linker.

Claim 39; Page 46-47; 55pp; English.

RESULT 1
AABO0158
ID AABO
XX AABO
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XX (US sCD4-SCFv(17b) is a neutralising bispecific fusion protein capable of binding to two sites of its target protein. The protein comprises a first binding domain capable of binding to an inducing site on the target protein, a second binding domain capable of forming neutralising complex with an induced epitope of the target protein and a linker connecting the binding domains. SCD4-SCFv(17b) comprises a soluble CD4 fragment (containing domains D1 and D2) fused to a single chain Fv portion of antibody 17b via a linker. SCD4-SCFv(17b), its variant, analogue or mimetic is used for inactivating gp120 protein of HIV, and

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ARESULT 2
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Best Local S
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                                                                             25-MAR-2003
09-JAN-2003
06-FEB-1991
                            Plasmid T4/LFA-3/AD gene product with C-terminal encoding phosphatidylinositol (PI) linkage signaling sequence.
   Plasma membrane binding affinity; micelle
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                                                                                                                                                                                                                                                  PPRYTFGQ-TRLEIKLVPRGSGHHHHHH
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(revised)
(first en
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   RESULT 3
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25-MAR-2003 09-JAN-2003 06-FEB-1991

(revised) (first en (revised)

entry)

AAR07606

standard;

protein; 318

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Matches
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Best Local Similarity
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                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 295 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Disclosure; Fig
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Phosphatidyl-inositol linkage signalling DNA sequence - lymphocyte function-associated antigen 3, used for prodr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                N-PSDB; AAQ06404.
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TWTCTVLQNQKKVEFKIDIVVLAFQKAS
                                                                                                          LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                       ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                  LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                  ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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/label= T4/LFA-3/AD gene product
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Pred. No. 6.2e-47;
0; Mismatches 0;
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1. of chimeric
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RESULT 4
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AC AAY3
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Best Local S
Matches 208
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Key
            AAY39825;
                                 AAY39825
                                                                                                                                                                                                                                                                                                                            Sequence 318
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Disclosure; Fig 5;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Phosphatidyl-inositol linkage signalling DNA sequence - d. lymphocyte function-associated antigen 3, used for prodn.
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                                                                                                                                                   LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                              MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                       LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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ilarity 100.0%;
Conservative (
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                                 protein;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                    53pp; English.
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ARESULT 5
AAY8328
ID AAY8
XX AAY8
AC AAY8
XC AAY8
XX T14-J
XX T4 9
XX ST4;
XW AIDS
XX AIDS
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Matches
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11-JUN-1991;
06-JUL-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                     This sequence represents the soluble human T4 protein of the invention of the invention of the soluble human T4 protein blocks the binding of HTV to T4+ cells is therefore useful for the treatment of AIDS. Monoclonal antibodies against the T4 protein may be used as vaccines for immunising subject
           sT4; glycoprotein; human immunodeficiency virus; HIV; block binding;
AIDS; treatment; inhibit; cell to cell spread; infection; fusion.
                                                                 14-JUL-2000
                                                                                                           AAY88328
                                                                                                                                                                                                                                                                                                                                                                                      Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  N-PSDB;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Human
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                                                                                                                                                                               TWTCTVLQNQKKVEFKIDIVVLAFQKAS
                                                                                                                                                                                                                      LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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immunisation; therapy.
                                                                                                            standard;
                                                                                                                                                                                                           LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKS1QFHWKNSNQ1K
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ilarity 100.0%;
Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COLUMBIA NEW YORK
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91US-00713564.
92US-00909021.
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                                           amino acid sequence
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Pred. No. 7.9e-47;
0; Mismatches 0;
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RESULT 6
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KW CD4;
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Best Local
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         patients. Administration of ST4 effectively inhibits the cell to cell spreading of HIV infection and also the fusion of HIV-infected T4 cells and non-infected T4 cells. The administration of T4 alleviates several symptoms associated with AIDS, and prevents the occurrence of new pathological changes. The ST4 glycoprotein is useful for the prophylaxis and treatment of patients with AIDS. It is also useful as a reagent to identify natural, synthetic or recombinant molecules which act as therapeutic agents or inhibitors of T4+ cell interactions and in diagnostic assays for detection T4 proteins or molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               glycosylated sT4 glycoprotein. Human Immunodeficiency virus (HIV) uses sT4 as a target receptor on T cells. The invention relates to glycosylated sT4 which functions by blocking the binding of HIV to T4 target cells, and can be used for the prophylaxis and treatment of AII
CD4; IgM; human; CD4Mmu; fusion protein; immunoglobulin; HIV; SIV; gp120; therapy; diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Soluble T4 glycoprotein useful for prevention and treatment of acquired immunodeficiency syndrome and for screening inhibitors of human immunodeficiency viral binding.
                                              CD4-IgM fusion
                                                                              09-JAN-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Col 11-16; 64pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             30-JUN-1992.
                                                                                                            AAB19509
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               This sequence represents the full length amino acid sequence of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maddon PJ,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-AUG-1986;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-OCT-1987;
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                                                                                                                                       AAB19509 standard; protein; 416 AA
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                                                                                                                                                                                                                                      TWTCTVLQNQKKVEFKIDIVVLAFQKAS
                                                                                                                                                                                                                                                                                 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                 LVFGLTANSDTHLLQGQSLTLTLESPPGSSP8VQCRSPRGKNIQGGKTLSVSQLELQDSG 180
                                                                                                                                                                                                                                                                                                                                                                                                                         MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
                                                                                                                                                                                                                                                                                                                                              ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                                                                         ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                                                                                                                                                                                    TWTCTVLQNQKKVEFKIDIVVLAFQKAS 208
                                                                                                                                                                                                                                                                                                                                                                                                         MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Chess L,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Conservative
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                                                                            (first
                                              protein CH4Mmu.
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100.0%; Pro
                                                                            entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 1064; DB 3; Pred. No. 7.9e-47; O; Mismatches O;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Length 394;
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RESULT 7
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ID AAY5
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23-JAN-1989;
09-JUN-1992;
12-APR-1993;
                                                                                                                                                                                                                                                                                                                         region (see AAA50662). Fusion protein CD4Mmu and a nucleic acid encoding it are claimed. Also claimed are a vector comprising the nucleic acid, and a method of producing the fusion protein in secreted form using a transformed host cell. The fusion protein may further comprise a therapeutic agent, radiolabel or NMR imaging agent. The fusion protein can be administered to an animal (including humans) for treatment of HIV or SIV infection, and can also be used in assays for HIV or SIV, imaging additional status. IgM fusion proteins such as CD4Mmu provide complement-
                                                                                                                                                                                                                                                                                     Sequence 416 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                         The present sequence is that of fusion protein CD4Mmu comprising the extracellular portion of CD4, which binds to HIV gpl20, linked at its Cterminus to the human IgM heavy chain. To obtain the fusion protein, DNJ encoding CD4 was linked to IgM DNA at the Mst2 site upstream of the CH1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Example 1; Col 41-50; 39pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      CD4-immunoglobulin fusion proteins, useful for targeting gp120 of HIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       N-PSDB; AAA50662
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181
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                                                                                                                                61 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GEN
                                                                     LVFGLTANSDTHLLQGQSLTLTLESSPGSSSPSVQCRSSPRGKNIQGGKTLSVSQLELQDSG
              TWTCTVLQNQKKVEFKIDIVVLAFQKAS 208
                                                      LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                               ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                                                                                 immunity
TWTCTVLQNQKKVEFKIDIVVLAFQKAS
                                                                                                                                                                      MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                                                                                                                                                              Conservative
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93US-00057952.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note= "CD4 extracellular region
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                                                                                                                                                                                                                           Score 1064; DB 3;
Pred. No. 8.3e-47;
0; Mismatches 0;
208
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AAY51080

standard; protein; 436

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RESULT 8
AAY88329
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AC AAY8
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Best Local
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23-JAN-1989;
09-JUN-1992;
12-APR-1993;
                                                                                                                                                                                                                                                                                                                                                        This invention describes a novel nucleic acid (I) encoding a fusion protein comprising a DNA sequence encoding amino acids 1-173 of CD4 (II) and a DNA sequence encoding a human immunoglobulin (Ig) heavy or light chain (III). The products pf the invention have anti-human immunodeficiency virus (HIV) activity and are capable of binding to gp120. The fusion protein is useful for treating human immunodeficiency virus (HIV) or similar immunodeficiency virus (SIV). This sequence represents the fusion protein CD4Mg which is constructed from CD4 linked to human IgM upstream of the CH1 region
 AAY88329;
                       AAY88329 standard; protein; 458 AA
                                                                                                                                                                                                                                                                                                                                      Sequence 436 AA;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Fusion protein useful
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Fusion protein; human; CD4; IgM; immunoglobulin; gp120; anti-human immunodeficiency virus; CD4Mg.
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DB; AAZ44063.
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                                                                                                 TWTCTVLQNQKKVEFKIDIVVLAFQKAS
                                                                                                                                                                                                  ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                MNRGVPFRHLLLVLQLALLPAATQGKKVVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
                                                                                  TWTCTVLQNQKKVEFKIDIVVLAFQKAS
                                                                                                                                 LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                  ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                  MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKS1QFHWKNSNQIK
                                                                                                                                                                                                                                                                                    39.9%; ilarity 100.0%; Conservative
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89US-00299596.
92US-00896781.
93US-00057952.
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                                                                                                                                                                                                                                                                                    0;
                                                                                                                                                                                                                                                                                   Score 1064; DB 3;
Pred. No. 8.7e-47;
0; Mismatches 0;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           of human immunodeficiency virus.
                                                                                                                                                                                                                                                                                                          Length 436;
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RESULT 9
AAB81502
ID AAB8
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AC AAB8

AAB81502 standard;

protein; 458

AAB81502;

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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                      This sequence represents the amino acid sequence of glycosylated sT4 glycopyrotein. Human immunodeficiency virus (HTV) uses sT4 as a target receptor on T cells. The invention relates to glycosylated sT4 which functions by blocking the binding of HIV to T4 target cells, and can be used for the prophylaxis and treatment of AIDS patients. Administration of sT4 effectively inhibits the cell to cell spreading of HIV infection and also the fusion of HIV-infected T4 cells and non-infected T4 cells. The administration of T4 alleviates several symptoms associated with AIDS, and prevents the occurrence of new pathological changes. The sT4 glycoprotein is useful for the prophylaxis and treatment of patients with AIDS. It is also useful as a reagent to identify natural, synthetic or recombinant molecules which act as therapeutic agents or inhibitors of T4 cell interactions and in diagnostic assays for detection T4 proteins
                                                                                                                                                                                                                                                                                                                               Sequence 458
                                                                                                                                                                                                                                                                                                                                                               or molecules
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Soluble T4 glycoprotein useful for immunodeficiency syndrome and for immunodeficiency viral binding.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21-AUG-1986;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    sT4; glycoprotein; human immunodeficiency virus; HIV; block binding; AIDS; treatment; inhibit; cell to cell spread; infection; fusion.
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                                                                                                                                                                                                                   1 MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK 60
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                                                                                  LVFGLTANSDTHLLQGQSLTLTLESPPGSSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                             MNRGVPFRHLLLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
TWTCTVLONOKKVEFKIDIVVLAFQKAS 208
                     TWTCTVLQNQKKVEFKIDIVVLAFQKAS
                                                              LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL 120
                                                                                                                              ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                                                                           39.9%; Score 1064; DB 3 ilarity 100.0%; Pred. No. 9e-47; Conservative 0; Mismatches
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Query Match
Best Local S
Matches 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence is human CD4. Human CD4 extracellular domains 1 and 2 were used in the construction of CD4 oligomerisation fusion proteins. The fusion proteins contain an oligomerisation domain that enables the proteins to bind to one another to form oligomers. The oligomers may be used in an invention relating to a method for screening for compounds with the ability to inhibit a low affinity receptor-ligand interaction. The method uses an interfacial optical assay, such as surface plasmon resonance (SPR). The method is useful for screening candidate compounds for the ability to inhibit interaction between MHC/peptide complex and Total receptor, and MHC/peptide complex and CD8 or CD4 co-receptor. The compounds identified by the above methods which interfere with T cell receptor binding to a particular HLA type molecule are useful as immune inhibit for for transfer of the compounds in the control of the complex and the compounds identified by the above methods which interfere with T cell receptor for transfer of the compounds in the complex and the compounds identified by the above methods which interfere with T cell receptor for transfer of the compounds in the complex and the compounds identified by the above methods which interfere with T cell receptor for transfer of the compounds in the complex and the compounds in the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Protein
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           inhibitors for treating carcinomas, autoimmune diseases such as multiple sclerosis, human immunodeficiency virus (HIV) infection, rheumatoid arthritis, Hashimoto's disease, insulin dependent diabetes, Good pasture's syndrome, uveitis, psoriasis and graft rejection
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26. .458
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The specification describes an antibody which is specific for an antigenic fragment of gp120. This antigenic fragment binds to DC-SIGN or is exposed upon gp120 binding of DC-SIGN due to concomitant conformational change. DC-SIGN is a receptor that is specifically expressed on dendritic cells and facilitates infection of T lymphocytes with HIV. DC-SIGN is identical to a HIV-1 gp120-binding C-type lectin. D-SIGN binds ICAM-3 (which is expressed constitutively on T lymphocytes) with high affinity. The antibody of the invention inhibits the trans enhancement of HIV entry into a T cell or macrophage facilitated by dendritic cells. The antibody is useful to treat or prevent HIV infection. The present sequence represents a human CD4 protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     An antibody for the treatment or prevention of HIV-infection comprises gpl20 portion which binds to DC-SIGN or is exposed upon gpl20 binding of DC-SIGN due to concomitant conformational chance
                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence
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cc hinge region polypeptide comprises: a wild-type human IgG1 immunoglobulin Cc hinge region polypeptide; a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from (a) having 3 or more cysteine residues; cc where the mutated human IgG1 immunoglobulin hinge region polypeptide contains 2 cysteine residues, where the first cysteine is not mutated; a c mutated human IgG1 immunoglobulin hinge region polypeptide, derived from CC day having 3 or more cysteine residues, where the mutated human IgG1 immunoglobulin hinge region polypeptide contains no more than one c cysteine residue; and a mutated human IgG1 immunoglobulin hinge region polypeptide, derived from CC polypeptide, derived from (a) having 3 or more cysteine residues; where c c the mutated human IgG1 immunoglobulin hinge region polypeptide contains no cysteine residues. The binding domain-immunoglobulin fusion protein is c capable of at least one immunological activity comprising antibody c dependent cell-mediated cytotoxicity (ADCC) and complement fixation. The binding domain polypeptide is capable of specifically binding to an antigen. Also included are an isolated polynucleotide encoding the binding domain-immunoglobulin fusion protein, a recombinant expression construct comprising the polynucleotide (operably linked to a promoter), a host cell transformed or transfected with a recombinant expression
                                                                                                                                                                                                                                                                                                                                                                                                                                      The invention relates to a binding domain-immunoglobulin fusion protein comprising a binding domain polypeptide that is fused to an immunoglobulin hinge region polypeptide, an immunoglobulin heavy chain CH2 constant region polypeptide that is fused to the hinge region polypeptide, and an immunoglobulin heavy chain CH3 constant region polypeptide that is fused to the CH2 constant region polypeptide. The
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             malignant condition; B-cell disorder; melanoma; carcinoma; sarcoma; rheumatoid arthritis; myasthenia gravis; Grave's disease; type I diabetes mellitus; multiple sclerosis; autoimmune disease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; SEQ ID NO 170; 157pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New binding domain-immunoglobulin fusion protein, useful for treating a subject having or suspected of having a malignant condition or a B-cell disorder, e.g. melanoma, Grave's disease or autoimmune disease.
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17-JAN-2002; 2002US-00053530.
03-JUN-2002; 2002US-0385691P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Binding domain-immunoglobulin fusion protein-associated protein
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01-NOV-2001;
26-NOV-2001;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Human;
                             GENBANK; P01730
                                                       WPI; 2003-268312/26
                                                                                                            Woolf C,
                                                                                                                                                                    (GEHO )
(FARB )
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                                                                                                                                                                                                                                                                                                                                                                    14-AUG-2002; 2002WO-US025765
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     pain; neuronal tissue; gene therapy; segmental nerve injury; chronic constriction injury; CCI;
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                                                                                                                                                                    GEN HOSPITAL BAYER AG.
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                                                                                                            D'urso D,
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                                                                                                                                                                                                                                                    2001US-0312147P.
2001US-0346382P.
2001US-0333347P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             injury; SNI; Chung.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry
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                                                                                                                                                                                                  CORP
                                                                                                            Befort K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SEQ ID NO 3351.
                                                                                                            Costigan
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RESULT 13
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           derivative or allelic variation of the nucleic acid sequence. Also
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New composition comprising two or more isolated polypeptides, useful for preparing a medicament for treating pain in an animal.
                                       WO2004042346-A2
                                                                                                                                                                                                                                                                           Protein encoded by mRNA of the invention #105.
                                                                                                                                                                                                                                                                                                                                                                                                                          ADP12495
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ADP12495 standard; protein; 458
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                                                                                                       Homo sapiens
                                                                                                                                                                                                                                                                                                                                                   12-AUG-2004
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100.0%;
                                                                                                                                                                       immune system;
sease; multiple
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Score 1064; DB 7; Pred. No. 9e-47;
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Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, xenotransplant rejection or mechanical organ replacement rejection, in a individual. The method is also useful in assessing the immune status of an individual. The methods are also useful in diagnosing and monitoring diseases that involve the immune system, e.g. rheumatoid arthritis, lung, inflammatory bowel diseases, multiple sclerosis, HIV/AIDS or viral, bacterial or fungal infection. The present sequence represents a protein that is encoded by the mRNA of the invention.
                            HIV-1 infection; human immunodeficiency virus-1; CD4+ cell; chimeric endoplasmic reticulum; ER retention; envelope protein gp160; T cell receptor CD3epsilon chain; C-terminal domain; CD4epsilon15; gene therapy; human; receptor.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The present invention relates to diagnosing or monitoring transplant rejection, e.g. cardiac or kidney transplant rejection, in an individual comprises detecting the expression level of one or more genes. The methods, system and kits are useful in diagnosing or monitoring
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Diagnosing or monitoring transplant rejection, e.g. heart, kidney, liver, pancreas, pancreatic islet, lung, bone marrow or stem cell transplant rejection, in an individual, comprises detecting the expression level of
                                                                                                                                                                                                                                                 04-DEC-2003
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20-DEC-2002; 2002US-00325899.
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                                                                                                                                                                                                                                                                                                                                                                      standard; protein; 473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                                                                                                                                                                                     chain chimeric protein CD4epsilon15, SEQ
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100.0%; Pred. No. 9e-47;
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                                                                                                                                                                                                                                                                                                                                                             The invention relates to a composition for the treatment or prevention of CC human immunodeficiency virus-1 (HIV-1) infection. The composition CC comprises CD4+ cells that have been transduced with a vector that encodes CC a chimeric CD4 molecule which is capable of being retained in the CC endoplasmic reticulum (ER). The invention also encompasses the use of a CC soluble protein factor produced by CP4+ cells that have been transduced CC with a vector encoding a chimeric CD4 protein, and the use of an CC expression system encoding a chimeric CD4 protein. The ER-localised CC chimeric CD4 molecule binds to the HIV-1 envelope protein gp150, CC resulting in HIV-1 retention in the ER and thereby preventing viral CC comprises CD4 fused to 15 amino acids of the C-terminal domain of the T CC cell receptor CD3epsilon chain; this chimeric CD4 molecule is designated CC CD4epsilon15 (ADA44807). A known chimeric CD4 of similar structure but CC compositions of the invention have an in trans effect on the replication of HIV-1, and may be used to treat and prevent HIV-1 infection. The CC present sequence represents the chimeric CD4 molecule CD4epsilon15, which is specifically claimed for use in compositions of the invention.
                                                                                                                                                                                                                                                                       Matches 208;
                                                                                                                                                                                                                                                                                                       Query Match
                                                                                                                                                                                                                                                                                                                                        Sequence 473 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Claim 5; Page 33-35; 43pp;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Composition for treating or preventing human immune deficiency virus, comprises CD4 chimeric protein having a protective effect in trans, or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Alarcon Sanchez BJ,
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                                                                                  LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
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                   TWTCTVLQNQKKVEFKIDIVVLAFQKAS 208
                                                                                                                                                       ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                 ILGNQGSFLTKGPSKLNDRADSRRSLWDQGNFPLIIKNLKIEDSDTYICEVEDQKEEVQL
                                                                                                                                                                                                 MNRGVPFRHILLVLQLALLPAATQGKKVVLGKKGDTVELTCTASQKKSIQFHWKNSNQIK
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/note= "Part of the C-terminal domain of the T cell
receptor CD3epsilon chain"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Spanish.
                                                                                                                                                                                                                                                                Score 1064; DB 7;
Pred. No. 9.3e-47;
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Matches 208
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The invention provides a fusion gene encoding a fusion protein that comprises an extracellular CD4 DNA sequence or its fragment which binds to HIV gp120 when fused to an immunoglobulin (Ig) chain and the DNA sequence of an Ig heavy or light chain, where the DNA sequence encoding the variable region has been replaced with the DNA sequence which encodes extracellular CD4 or its gp120 binding fragment. The fusion protein is capable of being secreted. The fusion proteins are useful for treating HIV or SIV infections in animals, preferably humans. They are also useful for producing medicaments which can be used for treating HIV or SIV infections. The present sequence represents the fusion protein infections in humans. The present sequence represents the fusion protein cD4Mmu where the CD4 is linked to human IgG1 at the Mst2 site upstream of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           New fusion gene encoding immunoglobulin-CD4 fusion proteins, useful in the treatment of HIV or simian immunodeficiency virus infections.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Example 1; Page 47-53; 89pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           474 AA;
                                                                                      LVFGLTANSDTHLLQGQSLTLTLESPPGSSPSVQCRSPRGKNIQGGKTLSVSQLELQDSG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         39.9%; Score 1064; DB 3; ilarity 100.0%; Pred. No. 9.3e-47; Conservative 0; Mismatches 0;
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